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Masuho,Y. TITLE Full-length cDNA sequences JOURNAL Patent: EP 1347046.43 339 24-SEP-2003; Research Association for Biotechnology (JP) FEATURES 1. 2178 Source /organism="Homo sapiens" /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" ORIGIN Query Match 73.6%; Score 1459.4; DB 6; Length 2178; Best Local Similarity 96.4%; Pred. No. 1e-307; Matches 1526; Conservative 0: Mismatches 1: Indels 56. Gars 1.	Control Cont	206 GGCCGGGGATCCCCAGCTGCTGGTCGGTTCCCGGGAGGCGCTTCATGTGG 26 606 GCGCTGCTTCTTCGTACGAGGCTCTGGCCGCCGCGGAAGGCGCCTTCATGTGG 26 606 GCGCTGCTTCTTCGTACGAGGCTCTGGCCGCCGCGCGAGAAGTGGTGGTG 66	Db 386 GACCGCAGCTGTGGCCAGAGCGGCGACTGGCACGCCACGCGCGCG	566 AGGACTGATGACCCCTAGCCTCTTCCTTCCATCGGGCCATTTCCCAGAGTGG 910 CACCGCGTTATTCAGACTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGTGG 626 CACCGCGTTATTCAGACTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGTTGC 970 CCACCTGGCTGATGCAACCAACAACTAGTAACTCGCTAAACTGGCCAAGAAGTTGC 970 CCACCTGGCTGGATGCAACCACAACAGCACAATCCTGGTAAACTGCCTGAGGGCACT 686 CCACCTGGCTGGATGCAACCAACAACAGCACAACCTGGTAAACTGCCTGAGGGCACT	1030 ATCAGGGACCAAGGTGATGCAACAAGAAGAATTCCTCCAACTGAACTTCCA 10 1030 ATCAGGGACCAAGGTGATGCTCCAACAAGAATTCCTCCAACTGAACTTCCA 10 1030 GAGGACCCGGAAGAGTTATCTGGTCCAACAGAATTCCTCCCAACTGAACTTCCA 10 1030 GAGGACCCGGAAGAGTTATCTGGTCCATGAGATTCTTCGTGGTGTGTGGTGATGTTCCC 11 1030 GAGGACCCGGAAGAGATTATCTGGTCCATGAGCCTTGTGGTGTGTGT
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TITLE NEDO human cDNA sequencing project JOURNAL Unpublished REFERENCE 2 (bases 1 to 2178) AUTHORS Isogai,T. and Yamamoto,J. AUTHORS Logali,T. and Yamamoto,J. AUTHORS Logali,T. and Yamamoto,J. AUTHORS Logali,T. and Yamamoto,J. AUTHORS Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusan-Kamatari, Kisarazu, Chiba 292-392-8012, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) COMMENT RECOMMENT RECOMMENT RECOMMENT RESPECT RESPECT	Key Technology Center etc.); 3 x 3 end only pass sequencing: Anny HRI, and Biotechnology center, National Institute of Technology and Evaluation, clone selection for full insert sequencing: HRI and Evaluation: HRI and RAB. FEATURES Location/Qualifiers Location/Qualifiers / coration/Qualifiers / consonism="Homo sapiens" / db xref="taxon:s966" / clone="BRAWH2011795"	/tissue type="brain" /clone_lib="BRAWH2" /note="foloning vector: pME18SFL3" 4651568 /note="unnamed protein product" /codon start=1 /protein id="BAC04422.1" /db_xref="G1:21753912" /tanslation="MAALRWWQENTAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASG /translation="MAALRWWQENTAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASG /translation="MAALRWWQENTAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASG /translation="MAALRWWQENTAAFGCHHSTQILVMCLRALSGTKVWRV IFHRAISOSGTRALFRPTISNDLKVAKKVAHLAGCHHSTQILVMCLRALSGTKVWRV SNXWRFLQLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLIQGKVSSVPYLLGVNNLEF	NULLPYIMKFPLNRQANRKETITEGLIASTILINITKEGVPLVVEEYLDNVNBEHDWKM LRNRMMDIVQDAFVYATLGAHANGGLPVYLYEFEHHARGIIVKPRTDGADHGDE MYFLFGGFFATGLSMGKEKALSLQMKYWANPARTGNPDGNLPCWPRYNKDEKYLQL DFTTRVGMKLKEKKWAFWMSLYCSQRPEKQRQF" ORIGIN 73.6%; Score 1459.4; DB 9; Length 2178; Best Local Similarity 96.4%; Pred; No. 1e-307;	1526; Conservative US26; Conservative US6 GGTGCTGCAGAGAGTCCTGGGGGGGGGGGGGGGGGGGGG	546 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Oy 702 100 386 GACCGCAGCTGTGGCCGGGGGGGGCGCGCGCGCGCGCGCG
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QY 1791 AGATGGCTTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGGCAATTCT 1850 Db	AX37590 AX37590 AX37590 AX37590 AX37590 DEFINITION Sequence 57 from Patent WO0168848. ACCESSION AX375900 AX375000 AX375900 AX37500 AX3	NCE 1 ORS BAKER.K.P., Chen, J., Desnoyers, L., Goddard, A., Godows, Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W., Zhang, Z. E. Secreted and transmembrane polypeptides and nucleic at the same NAL Patent: WO 0168848-A 57 20-SEP-2001; Genentech, Inc. (US) Location/Qualifiers	source 1.2456 1.245e="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" Ouery Match 51.1%; Score 1013; DB 6; Length 2456;	Conservative TGCCTTGCACACCAAG	Oy 284 CAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCTTCTCCAGACCT 343 DD 448 CAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCTTCTCCAGACT 507 Qy 344 CCTCTAGGTTCTCAGGTTTGAGCTCAGAACCCGGAGCCCTGGAAAGGAATCAGA 403	Db 508 CCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAAGGAATCAGA 567 Qy 404 GATGCTACCACCTACCCGCCTG	Qy 426	688 CCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCCTGGGGCCAGCTGGCCTCGATG 464 TACGTCAGCACCGGGAACGGTACAGTGGCTGCGCTTCAGCGAGGACTGTTGTACCTG	Oy 524 AACGIGTACGCCCGGCGCGCGCGCGCGAATCCCCAGTGCTGCTGGTTC 583

CTGCGC 763 ||||||| |CTGCGC 1047 36GTCTC 883 ||||||| 36GTCTC 1167 ragraac 943 ||||||| ragraac 1227 CCGAGAT 1483 ||||| CCGA--- 1683 TTCGGC 823 DACACAG 1003 DAACAAG 1063 ||||||| DAACAAG 1347 ATGAGC 1123 TTGCCT 1243 GTGGAG 1363 ||||||| GTGGAG 1566 ATGGAC 1423 GGGAAG 1183 |||||| GGGAAG 1467 TGGTTC 583 GCCGCC 643 CCTGAGC 703 GTCAAA 1543 ----- 1683. ----- 1530 ----- 1683 CCCTTC 1603 AAGATG 1303

GNLGSTSTPATTSAPSSGFGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLQG KQMHVGKTPIOVFLGVPFSRPPLGILAFAPPEPEPEWKGIRDATTYPPGGNSLALSPGW SAVARSRLTATSASRVQASLLPQPLSVWGYRCLQESWGQLASMYVSTRERYKMLRFSE DCLYLLNYVAPARAPAGDPQLPWWWFPGGASRYSTSGSDARBRKVYLPFLQHRL GIFGTLSTDDSHARGWGCLLDQMAALBAVQENTAAFGGDFGNYTLFGGSAGAMSISGL MMSPLASGLFHRAISQSGTALFRLFITSNPLKVAHLAGGNHNSTQILVNCLRAL SGTKVMRVSNKCMFLQLMFQRDPEIINWSPVVDGVVIPDDPLYLLTGGKVSSVPYL LGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNFMDIVQDATFVYATL QTAHYHRETPWGICPAGHATTRMKSTGSWILDQEWA"	Query Match 51.1%; Score 1013; DB 9; Length 2456; Best Local Similarity 78.2%; Pred. No. 2.5e-210; Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;	Qy 224 GGTGCCTTGCACAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGGAAAA 283 Db 388 GGTGCCTTGCACAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGGAAAA 447	Oy 284 CAGATGCATGGGGGAAGACACCCATCCAAGTCTTTTAGGAGTCCCCTTCTCCAGACCT 343	508 CCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAAGGAATCAGA 404 GATGCTACCACCTCCGCCTG	Db 568 GATGCTACCACCTACCGCTGGATGGAGTCTGGCTGTGGCGAGGTGAGTGCAGGTG 627 Qy 426	Oy 426	Oy 464 TACGTCAGCACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGT	QY 524 AACGTGCCGCGCGCGCGCGCGCGCGCGCGGGGATCCCCAGCTGCCAGTGATGGTTC 583 Db 808 AACGTGTACGCCGGCGCGCGCGCCGGGGATCCCCAGCTGATGGTCTGGTTC 867	Qy 584 CCGGGAGGGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGTCTGACTTGGCCGCC 643 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 644 CGCGAGAAAGTGGTGGTGTTTTTGGAGCACAGGCTCGGCATCTTCGGCTTCCTGAGC 703 Db 928 CGCGAGAAAGTGGTGCTGTTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGC 987	Oy 704 ACGACGACGACGACGAGGAAACTGGGGGCTGCTGGACCAGATGGCGCTCTGCGC 763	Qy 764 TGGGTGCAGGAGAACATCGCAGCAGCGAGCAACCCAGGAAATGTGACCCTGTTCGGC 823 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 824 CAGTCGGGGGGCCATGAGCATCTCAGGACTGATGATGTCACCCCTAGCCTCGGGTCTC 883	Qy 884 TTCCAICGGCCATTICCCAGAGTGGCACGCGTTAITCAGACTTTCATCACTAGTAAC 943	Qy 944 CCACTGAAAGTGGCCAAGAAGGTTGCCCACTGGCTGGATGCAACCACAACAGAG 1003
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KEYWORDS SOURCE ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) REFERENCE AUTHORS Buldaryota, Netazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE Lal, Pr. Lee, S., Lu, D.A., Lu, Y., Patterson, C., Ramkumar, J., Ring, H.Z., Sanjanwala, M.S., Tang, Y.T., Thornton, M. and Tribouley, C.M. TITLE JOURAL TITLE JOURNAL Lal, Prof. (US) Location/Qualifiers Source Organism="Homo sapiens" //db_xref="taxon:9606" //db_xref="taxon:9606" //note="Incyte ID No: 7473869CB1"	Query Match Best Local Similarity 100.0%; Pred. No. 4.1e-186; Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 426 GGTGCCTGCAGGAGTCCTGGGGCCTGCCTCGATGTACGTCAGCACGCGGAACGGT 485	Oy 486 ACAAGTGGCTGTTCAGCGAGGACTGTTGTACCTGAACGTGTACGCGCGGCGCGGCG 545	Qy 546 CGCCGGGGATCCCCAGCTGCTGCTCTGGTTCCCGGAGGCGCCTTCATCGTGG 605 L	Oy 606 GCGCTGCTTCTTCGTACGAGGGCTCTGGCCGCCCGCGGGAAAGTGGTGGTGT 665	Qy 666 TTCTGCAGCACGAGGCTCGGCATCTTCGGCTTCCTGAGCACGACGACGACGCGCGCG	Oy 726 GGAACTGGGGGCTGCTGGACGAGGCGGCTCTGGCGCTGGGGGAGAACATCGCAG 785	Oy 786 CCTTGGGGGAGACCCAGGAAATGTGACCCTGTTGGGCCAGGGGGCCATGAGCA 845	Oy 846 TCTCAGGACTGATGATGACCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCCAGA 905	Oy 906 GIGGCACCGCGITAITCAGACITITCATCACTAGTAACCCACTGAAAGIGGCCAAGAAGG 965	OY 966 TTGCCCACCTGGCTGGATGCAACCACACACACACAGATCCTGGTAAACTGCCTGAGGG 1025	QY 1026 CACTATCAGGAACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCCTCCCAACTGAACT 1085 Bb 1328 CACTATCAGGGACCAAGGTGATGCGTGTGCCAACAAGATGAGATTCCTCCCAACTGAACT 1387 QY 1086 TCCAGAAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGTGGTGGTGTGT 1145 Db 1388 TCCAGAAGAGCCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGTGGTGGTGGTGA 1147
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutelv
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Patent: WO 02068652-A 53 06-SEP-2002;
Location/Qualifiers
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Pred. No. 3.1e-121;
0; Mismatches 321;
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    1602
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 53 from Patent W002068652.
AX921060 1 GI:40214762
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TUNKRSI PLIFSEDCLYLNI YPPVDLAKKNRILPVWWTTGGGLMVGGASTYSGLVLSA
HENVVVTIGYRLGIMGYFSTGDEHSRGWGLLDQVAALRWVOENIANFGGNPGSVTI
FORSAGGIVSTRULFRFATSESGYALITALVKKOKNDJAQQIAFPGCKN
TTSATVRCLRQKTEELLEISRKMKFFTIDLYGDSRENHAFLPIVVDGVLLPKMPEE
LILAEKKRNFVPYIGINKHFFGCLLPKLMGYPLSGREGKLDQKTAMSLLMKSCPIIGIPE
BLPLAARXYECTGODDPWYKKOLFLEYLGDANFGVEYPWTGTQY
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HPSFSSDMKPKTLIGDHGDELYSVFGAPFLKGGASEERIRJSKTMRMKFWANFARSGNP
NGEGLPSWPAYDQXEGYLQIGATTQPAQKLKDKEVAFWTELLAQGAAKKPPHKEHVEL
                                                           Loases in College, Taira, H. and Yamashita, T. Direct Submission
Direct Submission
Submitted (19-OCT-2002) Masao Miyazaki, Iwate University,
Department of Agro-bioscience, Faculty of Agriculture; 3-18-8 Ueda,
Morioka, Iwate 020-8550, Japan (E-mail:cdg83700@par.odn.ne.jp,
Tel:81-19-621-6157, Fax:81-19-621-6177)
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Pred. No. 4.2e-84;
0; Mismatches 631;
      feline liver
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/protein_id="BAC75712.1"
/db_xref="G1:30038513"
                                                                                                                                                                                                                                           /organism="Felis catus"
/mol_type="mRNA"
/db_xref="taxon:9685"
/sex="male"
                                                                                                                                                                                                                                                                                                                           /tissue_type="liver"
/dev stage="adult"
1. .1985
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larity 57.1%;
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    Molecular cloning of
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GEGIPSWPAYDQKEGYLQIGIPTQPAQKLKSKEMAFWTEILAKRAAEKLSPTEHVEL"
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis
                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (11-FBB-1999) Masakiyo Hosokawa, Chiba University,
Submitted (11-FBB-1999) Masakiyo Hosokawa, Chiba University,
Faculty of Pharmaceutical Sciences; 1-33 Yayoi-cho, Chiba,
263-8822, Japan (E-mail: masakiyo@p.chiba-u.ac.jp,
Tel:81-43-290-2921, Fax:81-43-290-2921)
Location/Qualifiers
         complete
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Purification, molecular cloning, and functional expression of liver microsomal acyl-CoA hydrolase: a member of the carboxylesterase multigene family Arch. Biochem. Biophys. 389 (2), 245-253 (2001)
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  familiaris CESdD1 mRNA for carboxylesterase D1,
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                              AB02329.1 GI:14331124
carboxylesterase D1; Dog liver carboxylesterase
Canis familiaris (dog)
Canis familiaris
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Pred. No. 1.6e-83;
0; Mismatches 657;

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    forganism="Canis familiaris"
    /mol_type="mRNA"
    db_xref="taxon:9615"
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/gene="CESdD1"
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Matches 868; Conservative (
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Direct Submission
Submitted (02-DEC-1997) Molecular Pharmacology, St. Jude Children's Research Hospital, 332 North Lauderdale, Memphis, TN 38105, USA
Location/Qualifiers
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larity 57.2%; Pred. No. 7.1e-83;
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TISAWAHCIROKTEELLETTIKKKELSLDIQGDPRESQPLLGTVIDGMLLLKTPEE
LQAERNFHTVPYMYGINKQBEGWLIPMLMSYPLSEQLDQKTAMSLLWKSYPLVCIAK
ELIPEATEXKYLGGTDDTVKKKOLFLDLADVNFGVBSVIVARHRDAGAPTTVYPER
RPGFSSDMKRYTVGOHGDELFSYFGAPFLKEGASEBEIRLSKOMVMKFWANDRANGNP
NGEGLPHWPEYNQKEGYLQIGANTQAAQKLKDKEVAFWTNLFAKKAVEKPPQTEHIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRKENI PLKLSEDCLYLNI YTPADLTKKNRL PVMVWI HGGGLMVGAASTYDGLALAAH
ENVVVVTI QYRLGI MGFFSTGDEHSRGNWGHLDQVAALRWVQDNI ASFGGNFGSVTI F
GESAGGESVSVLVLSPLAKNLFHRAI SESGVALTSVLVKKGDVKPLAEQIAI TAGCKT
                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 21 Row: m Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16905523. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product="crEs1 protein"
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/translation="WRIPAUVIATLAASAAWGHPSSPPWVDTVHGKVLGKFVSLEGFA
OPVAIFIGEPPARPPLGPLARPQPAEPWSFVKNATSYPPMCTQDPKAGQLLSELFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267
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                                                                                                                                                                                                                                                                                           Loulseged,
                                                                                                                                                                                                                                                                                                                           D.M., Nanavati,
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                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="synonyms: CES2, HMSE, HMSE1, SES1, CEH"
/db_xref="LocusID:1066"
/db_xref="MIM:114835"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9; Length 1975;
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/note="COesterase; Region: Carboxylesterase"
/db_xref="CDD:pfam00135"
                                                                                                                                                                           Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue type="Lung, large cell carcinoma"
|clone_lib="NIH_MGC_68"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTTTTTAGGAGTCCCCTTCTCCAGACCTCCTCTAGGTATCCTCAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:9220 IMAGE:3879691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Vector: pCMV-SPORT6'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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lab host="DH10B"
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Homo sapiens (Iuumaii)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaliai, Eutheria; Primates; Catarrhini; Hominidae; Homo.
I Dases 1 to 1975)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shemmen,C.M., Schuler,G.D.,
Altschul,S.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bossak,S.A., McEwan,P.J.,
McKernan,K.J., Mullahy,S.J., Bossak,S.A., McEwan,P.J.,
Villalon,D.K., Mullahy,S.J., Bossak,S.A., McEwan,P.J.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergen,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
Boutfard,G.G., Blakesley,R.W., Touchman,J.W., Schenko,Y.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequence
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1280 TTATTTGGTGCCCATCTGTGAATGTGGCTCGTCACCACACAGAGATGCTGGAGCCCCCACC 1339
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Direct Submission
Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
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Homo sapiens carboxylesterase 1 (monocyte/macrophage serine
esterase 1), mRNA (cDNA clone MGC:9220 IMAGE:3879691), complete
                                                                                                                                                                                                                                                                                                                           1616 TCCATGGGTAAGGAGAAGGCACTTAGCCTCCAGATGATGAATACTGGGCCAACTTTGCC
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                                                                                          TACCTGTATGAATTTGAGCACCACGCTCG----TGGAATAATCGTCAAACCCCGCACTGAT
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The present sequence, the coding region of which is also claimed, is that of human cDNA clone Fbh18903, which encodes carboxylesterase-2 (COE-2,

Claim 1; Page 119-122; 129pp; English.

cancer.

Novel isolated human carboxylesterase-2 family member polypeptide, 18903, useful for treating inflammatory disorders, pain disorders, tumor and

481 ACGCG 541 GCGCG 601 CGTGG 601 CGTGG 601 CGTGG 61 GCTGT 721 GCGCG 721 GCGCGCG 721 GCGCG 721 GCGCGC 721 GCGCG 721 GCGCGC 721 GCGCGC 721 GCGCGC 721 GCGCGC 721 GCGCGC 721 GCGCGC 721 GCGCGC 721 GCGCGC 721 GCGCGC 721 G		1081 GAACT 	1201 CCTTC 1201 CCTTC 1261 GCTAA 1261 GCTAA 1321 CCTGT	
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see ABB79484), a novel carboxylesterase family member. COE-2 participates in the metabolism of various lipid and fatty acid compounds which are involved in pain and/or inflammation signalling. It is highly expressed in tissues which contain afferent neurons, particularly brain and spinal cord tissue. The invention provides CDE-2 nucleic acid molecules, antisense nucleic acid molecules, recombinant expression vectors, host cells, transgenic animals, isolated CDE-2 proteins, tusion proteins, antigenic peptides and anti-CDE-2 antibodies. CDE-2 nucleic acids are used in claimed methods of identifying subjects having, or at risk of developing, an inflammatory or pain disorder. Compounds capable of treating an inflammatory or pain disorder. Compounds capable of ability to modulate COE-2 nucleic acid expression or COE-2 polypeptide activity. Modulator compounds are used in a claimed method of treating an inflammatory or pain disorder. Carboxylesterase-associated pain disorders include hyperalgesia, pain associated with musculoskeletal disorders include hyperalgesia, pain associated with musculoskeletal disorders and pain associated with surgery, rheumatoid arthritis, somatoform disorders, fibromyalgia syndrome, etc. Carboxylesterase-associated pain disorders include viral infection, ulcerative colitis, crohn's disease, lung disorder, peritonitis, chronic observable promothitis, saccoidesis, selecoderma, uppulmonary disease, lung inflammatory appendicitis, septic shock, nephritis, amyloidosis, chronic observable promothitis, saccoidesis, selecoderma, lupus, polymyositerase-associated disorders include viral inflammatory disease, other carboxylesterase-associated disorders include unmours, cancer, aberrant blood clotting, misregulation of the sleep/wake cycle. COE-aberrant blood clotting misregulation of the sleep/wake cycle. COE-aberrant blood clotting misregulation of the sleep/wake cycle. COE-aberrant bloods and polypreptides are also useful in secrecing assacs, decection assays (e.g., chromosomal mapping, tissue typ	S Quer Sest Mato	AATTCGGCCGAGGCTCCCGCCCCAGTACTTGCTGGCGGGGATTAAATTCGGCCGGC	GATAAAAGIGIGCICACACACIGIAGACACGGCIACCAIGCCAICCACAGIGITIGCCAIC CACAGIGITGCCAICACCACCCCCCACAGGAGAGCTGGCTGGAGCATGAGGTGGATCT CACAGIGITGCCAICACTCCTGCCCACAGCAGGAGCTGGCTGGAGCATGAGGTGGATTCT GTGCTGGAGCCTCACCCCTGCTGCTGATGGCGCAAGGGGCCTTGGGTGCATTCT GTGCTGGAGCCTCACCCCTCTGCTGATGGCGCAAGGGCCTTGGGTGCCTTGCACCAA GTGCTGGAGCCTCACCCCTCTGCTGATGGCGCAAGGCCCTTGGGTGCCTTGCACCAA GTGCTGGAGCCTCACCCCTCTGCTGATGGCGCAAGCGCCTTGGGTGCCTTGCACCAA	241 GAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGGAAAACAGATGCATGTGGGGAA 300 241 GAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGGAAAACAGATGCATGTGGGAA 300 241 GAGCCCTCAAGTGTTTTTAGGAGTCCCCTTCCCAGGTATCCTCAG 360 301 GACCCCATCCAAGTCTTTTTAGGAGTCCCCTTCTCAGGTATCCTCAG 360 361 GATTGCACCTCCAGAACCCCGGAGCCCTGCAACGAACCACCCTCTCAGGTATCCTCAG 360 361 GTTTGCACCTCCAGAACCCCGGAGCCCTGGAAAGGAATCAACATCCTACCTCACC 420 361 GTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAAGGAATCAAGAATCAACATCATACCC 420 421 GCCTGGGTGCCTGCAGACCCCTGGAGCCCTGGAAGGAATCAAGAGATGCTACCCCTACCC 420 421 GCCTGGGTGCCTGCAGAGCCCTGGAGCCTGGACTCTACCCCTACCC 480 481 ACGGTACCTGCAGGAGCCTTGGGGCCAGCTGGACTCTGAACGAAGGAA 480 481 ACGGTACAAGTGCTCAGGGAGACCTTGACCTGAACGTCAGCACGCGGAA 480 481 ACGGTACAAAGTGCTCAGGGAAGCAACTGTACCTCAACCTCAACCGCCGGC 540 [
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The invention relates to an isolated human drug metabolising enzyme (DME)

polypeptide or a biologically active or immunogenic fragment of DME. DME

containmune/inflammatory, developmental, endocrine, eye, metabolic and

autoimmune/inflammatory, developmental, endocrine, eye, metabolic and

cautoimmune/inflammatory, developmental, endocrine, eye, metabolic and

containmanetory discress including live disorders. Autoimmune/

containmatory dispress syndrome, addison's disease, atherosclerosis,

adult respiratory distress syndrome, Addison's disease, atherosclerosis,

allergies, anaemia, asthma, autoimmune haemolytic anaemia, autoimmune

controlatis, cronn's disease, atopic dermatitis, diabetes mellitus,

conflicts, uveitis, viral, bacterial, protozoal, parasitic,

conflicts, uveitis, viral, bacterial, protozoal, parasitic,

include cancer, arteriosclerosis, cirrhosis and psoriasis, desorders

controled epilepsy and cararct; and endocrine disorders

include epilepsy and cararct; and endocrine disorders

disorders of hypothyroidism including goitre, Grave's disease,

consociated with hypothyroidism including goitre, Grave's disease,

conformatic disorders associated with gonadal steroid hormones such as

endometriosis infertility, hypergonadal disorders and gynaecomastia.

Conformation disorders associated with gonadal steroid hormones such as

endometriosis, infertility, hypergonadal disorders and gynaecomastia.

Conformation disorders such as diabetes mellitus degeneration and

metabolic disorders associated with gonadal steroid hormones such as

conformed in fervillary, hypergonadal disorders and gynaecomastia.

Conformations of the eye include conjunctivitis and macular degeneration and

metabolic disorders include diabetes, cystic fibroais, obesity and

contery, hepatitis, constitation, diarrhoea, jaundice, wilson's disease,

chromboais and hepatic tumours. DMS gene is useful in gene therapy. The

contern hemosts and page and page en is useful in gene therapy.
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                                                                                                                                                                                 MR, Bruns CM, Das D, Delegeane AM, Ding L, Elliot VS;
AR, Griffin JA, Hafalia AJA, Khan FA, Lal P, Lee S, Lu DAM;
Patterson C, Ramkumar J, Ring HZ, Sanjanwala MS, Tang YT,
velu K, Thornton M, Tribouley CM, Walia NK, Warren BA, Yang J;
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                                                                                                                                                                                                                                                                                                                                                                                           New human drug metabolizing enzyme polypeptide and polynucleotide useful for diagnosing, treating and preventing cell proliferative, autoimmune/inflammatory, endocrine, eye, metabolic and gastrointestinal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 73; Page 172; 179pp; English.
18-AUG-2000; 2000US-0226440P.
24-AUG-2000; 2000US-0228067P.
31-AUG-2000; 2000US-023244P.
13-SEP-2000; 2000US-0234269P.
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P-PSDB; AAE21052.
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                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic codding sequences of the invention. Note: The sequence data for this pattent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at (II) at the printed specification, but was obtained in the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAAGTGGCTGCGCTTCAACGAGGACTGTCTGTACCTGAACGTGTACGCGCCGGCGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCCCGGGGATCCCCAACTGCCAGTGATGGTCTGGTTCCCGGGAGGCGCCTTCATCGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGACGACACACCACGCGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGCCTGCAGGAGTCCTGGGGCCAGCTGGCCTCGATGTACGTCAGCACGCGGGAACGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1532 BP; 348 A; 423 C; 441 G; 320 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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larity 93.5%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                      Claim 1; SEQ ID NO 10626; 103pp; English.
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Matches 1415; Conserv
P-PSDB; ABG10635
                                                                                                   biodiversity.
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344 CCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAAGGAATCAGA
                                                                                                                                                                                                                                   (GETH ) GENENTECH INC
                                                                                                                                                                                                                                               Wood WI, Goddard A,
                                                                                                                                                                                                                                                            WPI; 1999-551358/46.
P-PSDB; AAY41723.
                        06-MAY-1998;
07-MAY-1998;
07-MAY-1998;
07-MAY-1998;
                                                                07-MAY-1998;
07-MAY-1998;
13-MAY-1998;
                                                                                                                                   15-MAY-1998;
15-MAY-1998;
15-MAY-1998;
18-MAY-1998;
22-MAY-1998;
22-MAY-1998;
                                                                                            13-MAY-1998;
15-MAY-1998;
15-MAY-1998;
                                                                                                                15-MAY-1998;
15-MAY-1998;
15-MAY-1998;
                                                    07-MAY-1998;
07-MAY-1998;
                                                                                     13-MAY-1998
                                                                                                                                                                            22-MAY-1998
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28-MAY-1998
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                                      Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein; ss.
                          nucleotide sequence
                                                                                                                     98US-0077450P.
98US-0077641P.
98US-0077641P.
98US-0077649P.
98US-007060P.
98US-0078936P.
98US-0078936P.
98US-0078936P.
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98US-007864P.
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9805-0081070P
9805-0081071P
9805-008123P
9805-008123P
9805-0081817P
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9805-0082700P-
98US-0082704P-
98US-0082764P-
98US-0082767P-
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98US-0081955P.
98US-0082568P.
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98US-0083322P.
98US-0083392P.
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98US-0083500P
            (first entry)
                          Human PRO873
                                                                  sapiens
                                                                               WO9946281-A2
            07-DEC-1999
                                                                                                          08-MAR-1999;
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27-MAR-1998;
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01-APR-1998;
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                                                                                             16-SEP-1999
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                                                                                                                       10-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                           15-APR-1998
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29-APR-1998
                                      Human;
                                                                  Ношо
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The present invention describes secreted and transmembrane polypeptides and their polymucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood cogquiation disorders, cancers and cellular adhession disorders. They may also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders.
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98US-0083742P

98US-0084441P

98US-0084640P

98US-0084627P

98US-0084637P

98US-0084643P

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                       AACGTGTACGCGCCGGCGCGCGCCCGGGATCCCCAGCTGCCAGTGATGGTCTGGTTC
                                                                             CCGGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCC
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                                                                                                                                                      CGCGAGAAAGTGGTGCTGCTGCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGC
                                                                                                                                                                                                                             <u>ACGGACGACGACCCACGCGCGCGGGAACTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGC</u>
                                                                                                                                                                                                                                                                                                      TGGGTGCAGGAGACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTCGGC
                                                                                                                                                                                                                                                                                                                            TGGGTGCAGGAGAAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCACTGAAAGTGGCCAAGAAGGTTGCCCACCTGGCTGGATGCAACACAACAACAACAACAACAA
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                                                                                                                                                                                                                       KP, Botstein D, Desnoyers L, Eaton DL; F. Fong S, Gao W, Gerber H, Gerritsen ME; F. Grimeldi CJ, Gurney AL, Hillan KJ; Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL; Williams PM, Wood WI;
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.larity 78.2%; Pred. No. 6.6e-254;
Conservative 0; Mismatches 0;
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30-NOV-1999; 99WO-US028313.
02-DEC-1999; 99WO-US028551.
02-DEC-1999; 99WO-US020095.
16-DEC-1999; 99WO-US031243.
30-DEC-1999; 99WO-US031243.
30-DEC-1999; 99WO-US031274.
06-JAN-2000; 2000WO-US000277.
06-JAN-2000; 2000WO-US000277.
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Ferrara N, Filvaroff E, F
Goddard A, Godowski PJ, G
Kljavin IJ, Kuo SS, Napie
Stewart TA, Tumas D, Will
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Matches 1446; Conserv
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78.2%; Pred. No. 6.6e-254;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Fig 57; 774pp; English.
                                                                                                                                                                                                                                                                                                             , Chen J, Desnoyers I
Smith V, Watanabe CK,
                               200005-0201516P.
200000-US013705.
200000-US014042.
200000-US0150564.
200000-US015264.
                                                                                                                                                                               24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US032952.
01-DEC-2000; 2000WO-US032878.
20-DEC-2000; 2000WO-US033878.
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P-PSDB; AAU29052.
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                                                                    22-MAY-2000; 2
30-MAY-2000; 2
02-JUN-2000; 2
               25-APR-2000;
03-MAY-2000;
17-MAY-2000;
                                                                                                                      05-JUN-2000;
28-JUL-2000;
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                                                                                                                                                                                                                                        GAGAAGAAGATGGCTTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGG
                                                                                                                                                                                                                                                                         CAATTCTAAGGGTGGCTATGCAGGAAGGAGCCAAAGAGGGGGTTTGCCCCCACCATCCAGG
                                                                                                                           AACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGGCATGAAGCTCAAG
                                                                                                                                                         AACAAGGATGAAAAGTACCTGCAGCTGGATTTTTACCACAAGAGGTGGGCATGAAGCTCAAG
                                                                                        --- caaaccccaargarggaarcreccrecrecreccacecrac
                                                                                                                                                                                                    GGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGG
                                                     GCCAACTTTGCCCGCACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTAC
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                                                                                                                                                                                                                                                                                                                                                                        CCCTGGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTTCTACCCA 1953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human DNA encoding PRO polypeptide sequence #29.
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2000US-0190828P.
2000US-019007P.
2000US-0191048P.
2000US-0191314P.
2000US-0192655P.
2000US-0193032P.
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2000US-0189320P.
2000US-0189328P.
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11-APR-2000;
11-APR-2000;
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18-APR-2000;
25-APR-2000;
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primers for PRO polypeptides of the invention. The sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal! Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNY) alpha release from human bloom to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adernal, lung, colon, breast, prostate, rectal cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
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     Gurney AL;
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                                                                                                                                                                                                                                                                                                                Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals screen for modulators of the compounds.
L, Goddard A, Godowski PJ,
Wood WI, Zhang Z;
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PR 25-SEP-1998; 98US-0101786P. PR 29-SEP-1998; 98US-010240P. PR 29-SEP-1998; 98US-010230P. PR 29-SEP-1998; 98US-0102330P. PR 29-SEP-1998; 98US-0102331P. PR 30-SEP-1998; 98US-0102570P. PR 30-SEP-1998; 98US-0102570P. PR 30-SEP-1998; 98US-0102570P. PR 30-CTT-1998; 98US-010258P. PR 01-OCT-1998; 98US-010268P. PR 02-OCT-1998; 98US-010349P. PR 06-OCT-1998; 98US-010349P. PR 06-OCT-1998; 98US-010349P. PR 07-OCT-1998; 98US-010349P.	Query Match Best Local Similarity 78.2%; Pred. No. 6.6e-254; Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;	Qy 224 GGTGCCTTGCACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGAAAA 283		OY 344 CCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAAGGAATCAGA 403	4 0	Oy 426	426	ACCTG ACCTG	524 AACGTGTACGCCGGCGCGCGCGCGCGAATCCCCAGCTGCCAGTGATCGTCTGGTTC 583			ACGGACGACGACGCCACGCGGGGAACTGGGGGTGCTGGACCAGATGGCGGCTTGGCGCTTGCTGGACACAGATGGCGGCTTTTGCGCGCTTGCTT	TGGGTGCAGGAGAACATCGCAGCCTTCGGGGAAACCCAGGAAATGTGACCCTGTTCGGC 	CAGTCGGCGGGGCCATGAGCATCTCAGGACTGATGATGTCACCCCTAGCCTCGGGTCTC	884 TICCAICGGGCCAITICCCAGAGIGGCACCGCGITATICAGACTITICAICACTAGIAAC 943

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17-AUG-1998;
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    Human, secreted and transmembrane protein: PRO, gene therapy, tumour necrosis factor-alpha release; TNN-alpha release; chondrocyte proliferation; chondrocyte differentiation; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
                                                                                                                    Novel human secreted and transmembrane protein PRO873 cDNA.
    ACA75528 standard; cDNA; 2456 BP
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				998US-0102684P. 998US-0102687P. 998US-0102687P. 988US-0102687P. 11arity 78.2%; Pred. No. 6.6e-254; Conservative 0. Mismatches 0; Indels 403; Gaps CCCTTCCACACTAGAGGCCTCAAGTGGTCACAATATGGAACCTGCAAGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAA

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tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
tissue typing.
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tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
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998; 98US-0103449P. 51.1%; Score 1013; DB 7; Length 2456;. Similarity 78.2%; Pred. No. 6.6e-254; 5 Conservative 0; Mismatches 0; Indels 403; Gaps GGTGCCTTGCACCAAGAGGCTCAAGAGGTCAACAATATGGAACCTGCAAGAAAAAAAA	448 CAGATGCATGTGGGGAAAGACCCCATCCAAGTCTTTTTAGGAGTCCCCTTCTCCAGACCT 507 344 CCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGGAAAGGAATCAGA 403 508 CCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGGAAGGAA	GCACGATCTCGGCTCACTGCACCTCCGGGGTTCAAGCCAGGTCTCCTGGTGGGGGGTGGGGGGGG	TACGTCAGCAGCGGGAACGGTACAGGGCTTCAGCGAGGACTGTCTGT	808 AACGTGTACGCCGGCGCGCGCGCGCGCGCGGAGCTGCCAGTGATGGTCTGGTTC 867 584 CCGGGAGGCGCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGCTCTGACTTGGCCGCC 643	CGCGAGARAGIGGTGGTGTTTTGGGAGCTCGGCATTTTGGGCTTGGGGCTGGGGAGAGAGA	1048 TGGGTGCAGGAGAACAICGCAGCCTICGGGGGAGACCCAGGAAAIGTGACCCTGTICGGC 1107 824 CAGTCGGCGGGGCCAIGAGCATCTCAGGACTGATGTGACCCCTAGCCTCGGGTCTC 883	884 TTCCATCGGCCATTTCCCAGAGTGGCACCGCGTTATTCAGACTTTTCATCACTAGTAAC 943 1168 TTCCATCGGGCCATTTCCCAGAGTGGCACCGCGTTATTCATCATCACTAGTAAC 1227 1168 TCCATCGGGCCATTTCCCAGAGGTGCCACCGCTTATTCAGACTTTCATCACTAGTAAC 1227 944 CCACTGAAAGGTGGCCAACAAGGTTGCCCACCTGGTGGAACGAAC	1004 ATCCTGGTAAACTGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAG 1063

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qq	1684	1683
<i>λ</i> ο	1664	GCCAACTTTGCCCGCACAGGAAACCCCAATGATGGGAATCTGCCTGC
qq	1684	GADACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTAC 1724
č	1724	1724 BACBAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAG 1783
qq	1725	1725 AACAAGGATGAAAAGTACCTGCAGGATTTTACCACAAGAGTGGGCATGAAGCTCAAG 1784
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Title: Perfect score:

US-10-001-227-1 1983 1 cctttagccaattcggccga.....gtttaaacctgcaggactag 1983 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

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~	37-3	15-3		52A-1	106-1	26A-5	56-1	95-1	26A-7	56-5	95-5	26A-6	56-3	95-3	95-7	50-8	占	6		95B-2	3-1	18B-3	62-3		8-3	78-33	84A-2
	-09-264-7	-10-023-	-10-023-	-07-732-	-US92-(318-318	-08-370-	-08-814-	-08-318-	-08-370-	-08-814-	-08-318-	-08-370-	-08-814-	-08-814-0	-08-445-0	-08-204-6	-08-445-0	-08-204-6	-09-355-2	-08-370-2	0	-08-482-2	00183-1	-09-347-8	-09-347-8	-08-462-8
ü	Sn	ΩS	ΩS	nS	PCT	SD	us	us	OS.	ns	S	S	SD	us	Ġ	ΩŠ	us	nS	US	Ġ	Si	ns	nS	52	us	S	as
DB	<u> </u> m	4	4	ч	S	~	N	m	7	~	ო	7	7	m	m	Н	-	Н	-1	4	m	Н	Н	9	4	4	Н
Length	1701	1746	2158	1845	1845	2256	2256	2256	3016	3016	3016	3096	3096	3096	35060	2184	18	42	42	42	48	10	01	70	34	9	0
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Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli	שיחוֹ	Sequence 13, Appl Sequence 21, Appl Sequence 31, Appl	3,,	, 6, u	equence 5, equence 5, equence 3,	Sequence 3, Appli Sequence 2, Appli Sequence 1, Appli
1 US-08-461-881B-2 US-09-123-960-2 US-09-401-3667-5	US-09-491-356C- US-09-491-356C- US-09-491-356C-	1 US-09-058-260-13 1 US-09-058-260-21 1 US-09-058-260-31	-09-058	US-09-058-260-	2 US-08-781-802-5 3 US-08-694-078-5 2 US-08-781-802-3	3 US-08-694-078-3 3 US-09-103-840A-2 3 US-09-103-840A-1
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15;
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21.4%; Score 424; DB 3; Length 1701;
Best Local Similarity 57.0%; Pred. No. 4e-106;
Matches 860; Conservative 0; Mismatches 635; Indels 1!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Rabbit
US-09-264-737-3
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GENERAL INCURTIS.

APPLICANT: Silos-Santiago, Inmaculada

TITLE OF INVENTION: 5310, A NOVEL HUMAN CARBOXYLESTERASE

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-122001

CURRENT APPLICATION NUMBER: 60/10/23,515

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: 60/256,369

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-28

NUMBER OF SEQ ID NOS: 6

SOUTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LEMET. 1746
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                                                                                                                                                                                                                                         Sequence 3, Application US/10023515
Patent No. 6664091
GENERAL INFORMATION:
                                                                         GCTTTTTGGA 1805
                                                                                                                       1633 GCTTTCTGGA 1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-515-3
                                                                                                                                                                                              RESULT 2
US-10-023-515-3
                                                                         1796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACTICCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTG 1141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1039 ATGGTGGGAATCAACCAGCAAGAGTTTGGCTGGATTATCCCAATGCAAATGCTGGGCTAT 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1319 ACCCTGTTGAATATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGAGTACCTGGACAAT 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGATGGACATAGTTCAAGATGCC 1438
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GTGTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGACGACAGCCACGCG 721
                                                                                                                                                                                                                                                                                                                   GTGACCATTCAGTACCGCCTGGGCATCTGGGGATTCTTCAGCACAGGAGATGAGCACAGC
                                                                                              CGCGGGAACTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGCAGGAGAACATC
                                                                                                                                                                                       GCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTCGGCCAGTCGGCGGGGGCCATG
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APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: 00/10/023,515
CURRENT FILING DATE: 2001-11-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-16
PRIOR PELICATION NUMBER: 60/279,508
PRIOR PELICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PARTES 2001-03-28
SOFTWARE: FARTES 2001-03-28
SOFTWARE: FARTES 2001-03-28
SEQ ID NO: 6
SEQ ID 
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13.8%; Score 272.8; DB 4;
Best Local Similarity 53.0%; Pred. No. 1.1e-64;
Matches 812; Conservative 0; Mismatches 627;
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NAME/KEY: CDS

; LOCATION: (96)...(1838)

US-10-023-515-1
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ORGANISM: Homo sapiens
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Length 2158,

424 389 484 544

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AAGAAGGITGCCCACCIGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC 1018
687 GGGAACTGGGCCTTCAAGGACCAGGTGGCTGTTCTTGTCCTGGGTCCAGAAGAACATCGAG 746
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                                                                                              ATCTCAGGACTGATGTCACCCCTAGGCTCGGGTCTTCCATCGGGCCATTTCCCAG 904
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US-10-023-515-1
Sequence 1, Application US/10023515
Patent No. 6664091
GENERAL INFORMATION:
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Indels
COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/732,962A

FILING DATE: 19910722

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 3804/JPW/LSW

PREGISTRATION NUMBER: 38304/JPW/LSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 148.2; DB 1;
Pred. No. 1.3e-30;
0; Mismatches 693;
                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 393
REFERENCE/DOCKET NUMBER: 393
TELECOMMUNICATION INFORMATION:
TELERAX: (212) 664-6525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENOTH: 1845 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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NAME/KEY:
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IOCATION:
US-07-732-962A-1
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                       CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCCTCCAA 1078
                                                                                                                                                                               GCTTTCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCAATTCCT 1121
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| Patent No. 5248604
| GENERAL INFORMATION:
| TITLE OF INVENTION: EXPRESSION OF FITLE OF INVENTION: RECOMBINANT HUN NUMBER OF SEQUENCES: 2
| CORRESPONDER ADDRESSE: CORRESPONDER ADDRESSE: 30 Rockefeller Plaza | CITY: New York | CITY: New York | COUNTRY: USA
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US-07-732-962A-1
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545 GCGCCCGGGGATCCCCCAGCTGCAGTGATGGTCTGGTTCCCGGGAGGCGCCCTTCATCGTG
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
OPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06106
FILING DATE: 1992072
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. REGISTRATION NUMBER: 39:04-B-PCT/JPW/EAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 48.3%;
Matches 680; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: 1..1842
PCT-US92-06106-1
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                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/318,826A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.5%; Score 148.2; DB 2;
48.3%; Pred. No. 1.4e-30;
iive 0; Mismatches 693;
                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 2391
TELEPHONE: (248) 539-5050
INFORMATION: (248) 539-5055
INFORMATION SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2256 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 48.3
Matches 680; Conservative
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Michigan
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Patent No. 5891725
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sakut, Haim
APPLICANT: Eckerein, Fritz
TITLE OF INVENTION: Synthetic Antisense
TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
TITLE OF INVENTION: Containing Them
INTEREMENT OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Kohn & Associates
STREET: 30500 No. 5891725thwestern Hwy., Suite 410
CITY: Farmington Hills
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896 ATTICCCAGAGIGG-----CACCGCGTTATICAGACTITICATCACTAGTAACCCACTG 949
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US-08-318-826A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/370,156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 148.2; DB 2;
Pred. No. 1.4e-30;
0; Mismatches 693;
                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington,
STREET: P.O. Box 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APFILING DATE:
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: KOADH, KEDNECH IN SECRET REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-307
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TO COG-4071
                                                                                                                                                                                                                                                                                         ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2256 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5%;
nilarity 48.3%;
Conservative 0,
NUMBER OF SEQUENCES:
                                                                                                                          STATE: Michigan COUNTRY: 115
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US-08-370-156-1
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Best Local Simi
Matches 680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 950 AAAGTGGCCAAGAAGGTTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTG 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              988 CGCAGGGCCACGCAGCTGGCCCACCTTGTGGGCTGTCCTCCAGGCGGCACTGGTGGGAAT 1047
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AACGTGGCAGCCTTCGGGGGTGACCCCGACATCAGTGACGCTGTTTGGGGAGGGGCGCGGGA
                                                                                                                                                                                                                                                         896 ATTICCCAGAGIGG-----CACCGCGTTATICAGACTTITCATCACTAGTAACCCACTG
                                                                                                                                                                                                                                                                                                                                           928 GIGCIGCAGAGCGGIGCCCCCCAATGGACCCTGGGCCACGGTGGGCATGGGAGAGAGCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1048 GACACAGAGCTGGTAGCCTGCCTTCGGACACGACCAGCGCAGGTCCTGGTGAA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1339 grecesercesegrrececaseraasreacereseaacesaserereseretarrae
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Patent No. 5932780.
GENERAL INFORMATION:
APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Shani, Mosha
TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
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US-08-370-156-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
: 30500 No. 6025183thwestern Highway, Suite 410 Farmington Hills Michigan Y: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: HULLS: SINGLE
STRANDEDDESS: SINGLE
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "ACHE gene comprising exons
                                                                                                                                                                                                                                                                       Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 148.2; DB 3;
Pred. No. 1.4e-30;
0; Mismatches 693;
                                                                                                                                                                                                                                                                                                                        PARTICATION NUMBER: US/08/814,095
FILING DATE:
CLASSIFICATION
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECUPENCE: (248) 539-5555
TELEPACE: (248) 539-5555
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2256 base pairs TYPE: nucleic acid
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ORIGINAL SOURCE:
ORGANISM: HOT
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Patent No. 6025183
GENERAL INFORMATION:
APPLICANT: Sored, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Zakut, Haim
APPLICANT: ABIN, MOSHA
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
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CORRESPONDENCES:
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APPLICATION NUMBER: US/08/318,826A
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Pred. No. 1.6e-30;
0; Mismatches 693;
Oligodeoxynucleotides and Containing Them
                                                                                                                                                                                                                                     ADDRESSE: Kohn & Associates
STREET: 30500 No. 5891725thwestern Hwy.,
CITY: Farmington Hills
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KÖDI, KENDER: 30,955
REFERENCE/DOCKET NUMBER: 2391.
TELECHMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
INFORMATION: (248) 539-5050
INFORMATION: 728 SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3016 base pairs
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Best Local Similarity 48.3%;
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STRANDEDNESS: double
TOPOLOGY: linear
TITLE OF INVENTION: OI TITLE OF INVENTION: CO NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
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ZIP: 483
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Patent No. 5891725
GENERALINEOMATION:
APPLICANT: Sored, Hermona
APPLICANT: Sakut, Haim
APPLICANT: Eckstein, Fritz
TITLE OF INVENTION: Synthetic Antisense
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APPLICANT: Soreq, Hermona
APPLICANT: Saret, Haim
APPLICANT: Shani, Moshar
APPLICANT: Shani, Moshar
APPLICANT: Shani, Moshar
TITLE OF INVENTION: TEANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington, Barnard & Perry
STREET: P.O. Box 4330
                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.30
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Pred. No. 1.6e-30;
0; Mismatches 693;
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COMPUTER: INN PC compatible
COREATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: PETENTIN Release #1.0, Version #1
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,156
FILING DATE:
FILING DATE:
CLASSIFFCATION: 536
ATTORNEY AGENT INFORMATION:
NAME: KODIN, Kennerh I.
REGISTRATION NUMBER: 30,955
REFERENCE/DGCKET NUMBER: 9-9307 (Mulford)
TELECHOMYL (810) 689-350
TELECHOMYL (810) 689-4071
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3016 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
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IBM PC compatible
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Conservative
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STREET: 30500 No. 6025183thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
Sequence 5, Application US/08814095
Patent No. 6025183
GENERAL INFORMATION:
APPLICANT: Sakey, Hermona
APPLICANT: Sakey, Hermona
APPLICANT: Sakey, Hermona
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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4, 5 and 6"
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
RURRBNT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
FILING DATE:
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Pred. No. 1.6e-30;
0; Mismatches 693;
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Alternatively
DESCRIPTION: comprising exons 2, 3,
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ATTORNEY/ACENT INFORMATION:
NAME: MONEGOMERY, 11ene N.
REGISTRATION NUMBER: 38,972
REPERENCE/COCKET NUMBER: 2391.
TELECHONICATION INFORMATION:
TELEFAX: (248) 539-5050
INFORMATION FOR SEQ ID NO. 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3016 base pairs
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APPLICANT: Soreq, Hermona
APPLICANT: Eckstein, Fritz
TITLE OF INVENTION: Synthetic Antisense
TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
TITLE OF INVENTION: Containing Them
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Pred. No. 1.6e-30;
0; Mismatches 693;
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STREET: 30500 No. 5891725thwestern Hwy.,
CITY: Farmingcon Hills
STATE: Michigan
1696 AACTTTGCCCGCACAGGGGATCCCAATGA 1724
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APPLICATION NUMBER: US/08/318,826A
FILING DATE:
                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08318826A Patent No. 5891725
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGIETRATION UNDERE: 30,955
REFERENCE/DOCKET NUMBER: 2391.
TELECOMMUNICATION INFORMATION:
TELEPAX: (248) 539-5050
TELEPAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 3096 base pairs
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Best Local Similarity 48.3%;
Matches 680; Conservative
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Zakut, Haim
APPLICANT: Zakut, Haim
APPLICANT: Janit, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington, Barnard & Perry
STREET: P.O. Box 4390
CITY: Troy.
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Pred. No. 1.6e~30;
0; Mismatches 693;
                                                                                                                AACTITGCCCGCACAGGAAACCCCAATGA 1695
                                                                                                                                      AACTITGCCCGCACAGGGGATCCCAATGA 1724
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ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-307 (M
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 689-3500
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APPLICATION NUMBER: US/08/370,156
                                                                                                                                                                                                     RESULT 13
US-08-370-156-3
; Sequence 3, Application US/08370156
; Patent No. 5932780
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Best Local Similarity 48.3%;
Matches 680; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 3096 base pairs
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STRANDEDNESS: single
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, LOCATION:
US-08-370-156-3
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translated portion
1636 TCTCGAAACTACACGGCAGAGAAAATCTTCGCCCAGGGACTGATGCGATACTGGGCC 1695
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Pred. No. 1.6e-30;
0; Mismatches 693; Indels
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DESCRIPTION: /desc = "Alternatively spliced AChE
DESCRIPTION: comprising exons 2, 3, 4 and 5 as well
DESCRIPTION: of Intron 4 (readthrough)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sorie, Hermona
APPLICANT: Sorie, Harmona
APPLICANT: Zakut, Haim
APPLICANT: Zakut, Haim
APPLICANT: Zakut, Haim
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
NUMBER OF SEGUENCES: 7
ADDRESSEE: KOHN & ASSOCIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SULTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
FILING DATE:
                                                                                                                                                                                                                                                                                                  AACTITIGCCGGACAGAGGGATCCCAATGA 1724
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NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3096 base pairs
                                                                                                                                                                                                                                                            AACTITGCCCGCACAGGAAACCCCAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08814095 Patent No. 6025183
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, LOCATION:
US-08-814-095-3
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US-08-814-095-3
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STREET: 30500 No. 6025183thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sored, Hermona
APPLICANT: Sored, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
NUMBER OF SEQUENCES: 7
ADDRESSEE: KOHN & ASSOCIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /desc = "Cosmid including ACHE promotor, ACHE gene and ARS gene"
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ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Verr
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MOLIGOMETY, Ilene N.
REGISTRATION NUMBER: 38,91.00066
TELECOMMUNICATION INFORMATION:
TELEFRAX: (248) 539-5050
TELEFRAX: (248) 539-5056
TELEFRAX: (
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Patent No. 6025183
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7q22
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24344 CTGCCACCGGAGCCCAAGCAGCCTTGGTCAGGGGTAGACGCTACAACAACTTCCAGAGT 24403
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FEATURE: Exon
LOCATION: complement (32959..33094)
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OTHER INFORMATION: /number= 6
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OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 11
PEATURE:
LOAME KEY: exon
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 7
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OTHER INFORMATION: /gene= "AR"
POTHER INFORMATION: /number= 9
NAME/KEY: exon
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OTHER INFORMATION: /number= 10
FEATURE:
NAME/KEY: exon
LOCATION: complement (31131..31284)
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LOCATION: complement (30187..30274)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 14
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NAME/KEY: exon
LOCATION: complement (29664..29856)
COTER INFORMATION: /gene= "ARS"
COTHER INFORMATION: /number= 16
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                                            545 GCGCCCGGGGATCCCCAGTGCCAGTGATGGTCCCGGCAGGCGCCTTCATCGTG 604
24521 CGGCC--TACATCCCCCACCCCTGTCTCGTCTGGATCTATGGGGGTGCTTCTACAGT 24577
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Search completed: August 11, 2004, 18:18:24 Job time : 174.88 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description		ממחתנונע	Sequence 29,	Sequence	Sequence 339	Sequence 253	Sequence	Sequence	Sequence	Sequence 253	Sequence	Sequence	Sequence	Sequence	Sequence
ID	110 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	T - / 77 - TOO - OT - CO	US-10-343-593-29	US-10-001-227-3	US-10-108-260A-339	US-09-978-295A-253	US-09-978-697-253	US-09-978-192A-253	US-09-999-832A-253	US-09-978-189-253	US-09-978-608A-253	US-09-978-585A-253	US-09-978-191A-253	US-09-978-403A-253	US-09-978-564A-253
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% Query Match	000		97.3	88.4	73.6	51.1	51.1	51.1	51.1	51.1	51.1	51.1	51.1	51.1	51.1
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09-99	09-918-585A-2	-09-978-193A-2	-09-99	-09-978-187B-2	-09-978-643A-2	-09-97	-09-978-298A-2	-09-978-188A-2	-09-97	-09-978-194A-2	-09-99	-09-978-299A-2	6-60-	-09-978-6	8-876-60-	-10-164-749A-2	-10-206-5	-10-199-670-5	-10-201-858-	39-999-831A-	-10-205-890-5	-10-208-024-	-10-201-853-5	10-013-917A-	-10-174-58	10-176-483-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
APPLICANT: WARREN, Bridget A.; YANG, Junming; APPLICANT: YAO, Monique G.; YUE, Henry ITLE OF INVENTION: DRUG METABOLIZING ENZYMES FILE REFERENCE: PT-0185 USN CURRENT APPLICATION NUMBER: US/10/343,593 CURRENT FILING DATE: 2003-01-29 PRIOR FILING DATE: 2003-01-29 PRIOR FILING DATE: 2000-08-04 PRIOR FILING DATE: 2000-08-04 PRIOR FILING DATE: 2000-08-11 PRIOR APPLICATION NUMBER: US 60/224,728 PRIOR APPLICATION NUMBER: US 60/226,440 200-08-18 PRIOR APPLICATION NUMBER: US 60/226,067 PRIOR APPLICATION NUMBER: US 60/220,067 PRIOR FILING DATE: 2000-08-13 PRIOR FILING DATE: 2000-08-13 PRIOR PAPLICATION NUMBER: US 60/230,063 PRIOR FILING DATE: 2000-09-13 PRIOR APPLICATION NUMBER: US 60/232,244 PRIOR PLING DATE: 2000-09-13 PRIOR APPLICATION NUMBER: US 60/234,269 PRIOR FILING DATE: 2000-09-13 PRIOR PELICATION NUMBER: US 60/234,269 PRIOR FILING DATE: 2000-09-20 NUMBER PEEL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1928.6;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; NAMPKEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7478588CB1
US-10-343-593-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.8%;
Matches 1931; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138
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1 ATCAGAGATGCTACCACCTACCGCCTGGGTGCCTGCAGGAGTCCTGGGGCCAGCTGGCC 36	458 TCGAIGTACGTCAGCACGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGACTGTCTG 517	518 TACCTGAACGTGTACGCCGGCGCGCGCGCGGGGATCCCCAGCTGCCAGTGATGGTC 577	TGGTTCCCGGGAGGCGCTTCATCGTGGGGCGCTGCTTCTTCGTACGAGGCTCTCTGACTTG	491 1GGTICCCGGGAGGCGCCTICAICGIGGGCGCTGCTICTICGIACGAGGCTCGACTIG 540 . 638 GCGCCGGGAGAAAGIGGIGGTGGTGTTTCTGCAGCACAGGCTGGGCALCTTCGGCTTC 697 . 541 GCGCCGGAAAAGIGGTGCTGTTTTCTGCAGCACAGGCTCGGCATCTTCGGGTTC 600	CTGAGCACGACGACGCCACGCGCGGGAACTGGGGGCTGCTGGACCAGATGGCGGCT 	758 CTGCGCTGCGTGCAGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTG 817	818 TICGGCCAGICGGCGGGCCCATGAGCATCICAGGACIGAIGAIGICACCCCTAGCCICG 877	878 GGTCTCTTCCATCGGGCCATTTCCCAGAGTGGCACCGCGTTATTCAGACTTTTCATCATC 937	938 AGTAACCCACTGAAAGTGGCCAAGAAGGTTGCCCACCTGGATGGA	998 ACACAGATCCTGGTAAACTGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCC 1057	1058 AACAAGATGATTCCTCCAACTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCC 1117	AIGAGCCCTGTGGTGGATGGTGTGATCCCAGATGACCCTTTGGTGCTCCTGACCCAG 117	8 GGGAAGGTTTCATCTGCCCTACCTTCTAGGTGTCAACAACTGGGATTCAATTGGCTC 1 	TTGCCTTATATCATGAAGTTCCCGCTAAACCGGCAGGGATGAGAAAGGAAACCATCACT 			1418 ATGGACATAGTICAAGATGCCACTTTGGTGTATGCCACACTGCAGACTGCTCACTACCAC 1477.	1478 CGAGATGCCGGCCTCCCTGTCTACCTGTATGAATTTGAGCACCACGCTCGTGGAATAATC 1537
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Oy 1698 GGAATCTGCCCTGCTGCCACGCTACAACAAGGATGAAAGTACCTGCAGCTGGATTTTA 1757	1707 GGAATCTGCCCTGCTGCCCACCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTA	OY 1/56 CCACAAGAGTGGSCATGAAGGTCAAGGAGAGAGAGAGGCTTTTTGGATGACTCTGTACC 1817	QY 1818 AGTCTCAAAGACCTGAGAGCAATTCTAAGGGTGGCTATGCAGGAAGGA	OY 1878 AGAGGGGTTTGCCCCCACCATCCAGGCCCTCGGGACACTAGCCATGGACATACCTGGGGA 1937	OY 1938 CAACAGITCTACCCA 1952 DD 1947 CAACAGITCTACCCA 1961		GENERAL INFORMATION: APPLICANT: KAPELLER-LIBERMANN APPLICANT: SILOS-SANTIAGO		CORRENT FILLING DAIS: 2001-11-30 PRIOR APPLICATION NUMBER: 60/250929 PRIOR FILING DATE: 2000-11-30 NUMBER OF SEQ ID NOS: 7	SOFTWARE: FASTSEQ IOF WINDOWS VERSION 4.0 SOFTWARE: FASTSEQ IOF WINDOWS VERSION 4.0 LENGTH: 1752 TYPE: DNA	CMCANTLESH: HONGO SAPIENTS CMCANTLESH: NAME/KEY: CDS COCATION: (1) (1752) FF-10.001-207-2	Query Match Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 98 ATGCCATCCACAGTGTTGCCACAGTGTTGCCATCACTCCTGCCCACAGCAGGAGCT 157 Db 1 ATGCCATCCACAGTGTTGCCATCAAGTGTTGCCATCACTCCTGCCCACAGCAGGAGCT 60	CAGACG 		11010 11010 11010 11010		398 ATCAGAGATGCTACCACCTGCGGTGCCTGCAGGAGTCCTGGGGGCCAGTGGCC

1749 1465 1869 1569 1405 1389 1449 1225 1029 1089 1149 1209 1269 1329 1045 606 625 696 685 745 802 865 925 849 565 505 AGGACTGATGATGACCCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCCAGAGTGG GCAGGCGATGAGAAAGGAAACCATCACTAAGATGCTCTGGAGTACCCGCACCCTGTTGAA 1046 TATCACCAAGAAGAAGAACACTTGTGGTGGAGAGAATACCTGGACAATGTCAATGAGA CAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAAAAGTACCTGCAGCT CACGGGGTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGGTTGC CACCGCGTTATTCAGACCTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGTTGC ATCAGGGACCAAGGTGATGCGTGTCCAACAAGATGAGATTCCTCCAACTGAACTTCCA ATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCCTCCAACTGAACTTCCA TGTCAACAACCTGGAATTCAATTGGCTCTTGCCTTATATCATGAAGTTCCCGGCTAAACCG GCAGGCGATGAGAAAGGAAACCATCACTAAGATGCTCTGGAGTACCCGCACCCTGTTGAA TATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCA 1106 TGACTGGAAGATGCTACGAAACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTA 1450 TGCCACACTGCAGACTGCTCACTACCACCGAGATGCCGGCCTCCCTGTCTACCTGTATGA 1166 TGCCACACTGCAGACTGCTCACTACCACCGAGATGCCGGCCTCCCTGTCTACCTGTATGA GAAGGCACTTAGCCTCCAGATGATGAAATACTGGGCCAACTTTGCCGGACACAGAAACCC CAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAAAAGTACCTGCAGCT 1750 GGATTTTACCACAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTGGATGAG GGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTGGATGAG CCACCTGGCTGGATGCAACCACACAGCACACAGATCCTGGTAAACTGCCTGAGGGCACT GAGAGACCCGGAAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGTGATCCC TGACTGGAAGATGCTACGAAACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTA GAAGGCACTTAGCCTCCAGATGATGAAATACTGGGCCAACTTTGCCCGCACAGGAAACCC

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R AFFLICATION NUMBER: 60/079689
R APPLICATION NUMBER: 60/079689
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079683
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079728
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/07978
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079920
R APPLICATION NUMBER: 60/079920
R FILING DATE: 1998-03-30
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R APPLICATION NUMBER: 60/080105
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R FILING DATE: 1998-04-01
R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/080328
R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/080333
R FILING DATE: 1998-04-01
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R FILING DATE: 1998-04-01
R FILING DATE: 1998-04-08
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A APPLICATION NUMBER: 60/081817
R FILING DATE: 1998-04-15
R FILING DATE: 1998-04-15
R FILING DATE: 1998-04-15
R APPLICATION NUMBER: 60/081952
R FILING DATE: 1998-04-15
                                                                                                             R FILING DATE: 1998-03-20
A APPLICATION NUMBER: 60/079294
R FILING DATE: 1998-03-25
A APPLICATION NUMBER: 60/079656
R FILING DATE: 1998-03-26
A APPLICATION NUMBER: 60/079664
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A APPLICATION NUMBER: 60/081071

R FILING DATE: 1998-04-08

A APPLICATION NUMBER: 60/081195

R FILING DATE: 1998-04-08

A APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/081229
FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/082569
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APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
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1526 TCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCAGGAA 1585
                                                         1870 GGAGCCAAAGAGGGTTTGCCCCCCACCATCCAGGCCCTGGGGAGACTAGCCATGGACATA 1929
                                                                                              1586 GGAGCCAAAGAGGGGGTTTGCCCCCCCCCAGGCCCTGGGGAGACTAGCCATGGACATA 1645
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APPLICANT: Williams, P. Mickey,
APPLICANT: Wood, Williams, P. Mickey,
APPLICANT: Wood, Williams, P. Mickey,
TITLE OF INVENTION: Screted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT APPLICATION NUMBER: 09/918565
PRIOR PLILING DATE: 2001-10-15
PRIOR PILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-21
PRIOR PLING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR PLING DATE: 1998-03-11
PRIOR PRIOR PLING DATE: 1998-03-12
                                                                                                                                                                                                                 1646 CCTGGGGACAAGAGTTCTACCCA 1668
                                                                                                                                                                       1930 CCTGGGGACAAGAGTTCTACCCA 1952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L. Hillan, Kenneth J. Krlavin, Ivar J. Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                          Sequence 253, Application US/09978295A Patent No. US20020156006A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-03-13
APPLICATION NUMBER: 60/078886
FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/078936
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APPLICATION NUMBER: 60/078004
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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GGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGGAAAA 283 Indels 403; Query Match
51.1%; Score 1013; DB 9; Length 2456;
Best Local Similarity 78.2%; Pred. No. 2.7e-292;
Matches 1446; Conservative 0; Mismatches 0; Indels 403.

ATGAGATTCCTCCAACTGGAACTTCCAGAGAGCCCGGAAGAGATTATCTGGTCCATGAGC 1123 TGGGTGCAGGAQAACATCGCAGCCTTCGGGGAQACCCAGGAAATGTGACCCTGTTCGGC 823 CCTGTGGTGGATGGTGTGGTGATCCCAGATGACCCTTTGGTGCTCCTGACCCCAGGGGAAG ATCCTGGTAAACTGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAG CGCGAGAAAGIGGIGGIGGIGITITCIGCAGCACAGGCICGGCAICTICGGCTICCIGAGC GTTTCATCTGTGCCCTACCTTCTAGGTGTCAACCTGGAATTCAATTGGCTCTTGCCT CCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAAGGAATCAGA 868 CCGGGAGGCCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCC CAGTCGGCGGGGGCCATGAGCATCTCAGGACTGATGATGTCACCCCTAGCCTCGGGTCTC 688 CCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCCTGGGGGCCAGCTGGCCTCGATG CCGGGAGGCCCTTCATCGTGGCCCCTTCTTCGTACGAGGCCTCTGACTTGGCCGCC CAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTAGGAGTCCCCTTCTCCAGACCT CAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTAGGAGTCCCCTTCTCCCAGACCT 628 GCACGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGCCTCAG GATGCTACCACCTACCGCCTG-------g 8 6 8 6 qq ò 엄 5. ò 엄 8 8 8 8 8 6 B 6 요 상 요 8 B 8

APPLICANT: Kuo, Sophia S. APPLICANT: Napier, Mary A. APPLICANT: Pan, James; APPLICANT: Pan, James; APPLICANT: Roy, Margaret Ann APPLICANT: Roy, Margaret Ann APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A. APPLICANT: Wood, Williams, P. Mickey APPLICANT: Wood, William I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Societed and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630PLC27 CURRENT FILING DATE: 2001-10-16 PRIOR PILICATION NUMBER: US/0919685 PRIOR PLICATION NUMBER: 09/918585 PRIOR APPLICATION NUMBER: 09/062260		PRIOR FILING DATE: 1998-03-27 PRIOR PLING DATE: 1998-03-27 PRIOR APPLICATION NUMBER: 60/079663 PRIOR PLING DATE: 1998-03-27 PRIOR PLING DATE: 1998-03-27 PRIOR FILING DATE: 1998-03-27 PRIOR FILING DATE: 1998-03-27 PRIOR FILING DATE: 1998-03-27 PRIOR FILING DATE: 1998-03-30 PRIOR FILING DATE: 1998-03-30 PRIOR FILING DATE: 1998-03-30 PRIOR FILING DATE: 1998-03-30 PRIOR FILING DATE: 1998-03-31
1468 GTTTCATCTGTGCCCTACCTTCTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCT 1244 TATATCATGAAGTTCCGGCTAAACCGGCAGGCGATGAGAAGCAAACCATCAGTGGTGT 1528 TAT	1984 GCCGGCCTCCCTGTCTCCTGTATGAATTTGAGCACCACGCTCGTGGAATAATTCGTCAAA 1543 1684	RESULT 6 US-09-978-697-253 Sequence 253, Application US/09978697 Patent No. US2000169284A1 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin P. APPLICANT: Bactein, David APPLICANT: Becsein, David APPLICANT: Becsein, David APPLICANT: Branch Resolution APPLICANT: Ferrara, Napoleon APPLICANT: Firanch Resolution APPLICANT: Firanch Resolution APPLICANT: Gao, Wei-Olang APPLICANT: Gao, Wei-Olang APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANT: Gurney, Austin L. APPLICANT: Gurney, Austin L. APPLICANT: Hillan, Kenneth J. APPLICANT: Kljavin, Ivar J.

224 GGTGCCTTGCACACAAGAGGCCTCAAGTGGTCACCAATATGGAACCCTGCAAGGAAAA 283
188 GGTGCCTTGCACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGAAAA 447 CCGGGAGGCGCCTICATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCC 643 404 GATGCTACCACCTACCGCCTG----- 425 426 628 GCACGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGCCTCAG 687 524 AACGIGTACGOGCGGCGCGCGCCCGGGAICCCCAGCTGCCAGTGAIGGICTGGTTC 583 Query Match 51.1%; Score 1013; DB 9; Length 2456; Best Local Similarity 78.2%; Pred. No. 2.7e-292; Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
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AACAAGGATGAAAAGTACCTGCAGCTTGATTTTACCACAAGAGTGGGCATGAAGCTCAAG	1784	OY 1844 CAATTCTAAGGGTGGCTATGCAGGAAGCCAAAGGGGGTTTGCCCCCACCATCAGG 1903	Qy 1904 CCCTGGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTTCTACCCA 1952 	RESULT 7 US-09-978-192A-253 ; Sequence 253, Application US/09978192A	; Patent No. US20020177553A1 ; GENERAL INFORMATION: ; APPLICANT: Bakerati, Avi ; APPLICANT: Baker Kevin P.	; APPLICANT: Botstein, David ; APPLICANT: Desnoyers, Luc ; APPLICANT: Eaton, Dan ; APPLICANT: Ferrara, Napoleon		; APPLICANT: Gerritsen, Mary E. ; APPLICANT: Goddard, Audrey ; APPLICANT: Godowski, Paul J. ; APPLICANT: Grimaldi, J. Christopher			; APPLICANT: Shelton David L.; APPLICANT: Stewart, Timothy A.; APPLICANT: Trumas, Daniel ; APPLICANT: Trumas, Daniel ; APPLICANT: Williams, P. Mickey; APPLICANT: Williams, P. Mickey	, APPLICANT: Wood, William I. ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ; TITLE OF INVENTION: Acids Encoding the Same ; FILE REPERENCE: PASSOPICS	; CURRENT APPLICATION NUMBER: US/09/978,192A ; CURRENT FILING DATE: 2001-10-15 ; PRIOR APPLICATION NUMBER: 09/918585 ; PRIOR FILING DATE: 2001-07-30	; PRIOR APPLICATION NUMBER: 60/062250 ; PRIOR FILING DATE: 1997-10-17	; PRIOR APPLICATION NUMBER: 60/064249 ; PRIOR FILING DATE: 1997-11-03 ; PRIOR APPLICATION NUMBER: 60/06511	PRIOR FILING DATE: 1997-11-13 FRIOR PELLING DATE: 1007-11-21 FRIOR FILING DATE: 1997-11-21	; PRIOR APPLICATION NUMBER: 60/077450 ; FRIOR FILING DATE: 1998-03-10	; PRIOR APPLICATION NUMBER: 60/077632 ; PRIOR FILING DATE: 1998-03-11 ; PRIOR APPLICATION NUMBER: 60/077641	FILING DATE: 1998-03 APPLICATION NUMBER: FILING DATE: 1998-03
868 CCGGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCC 927	928 CGCGAGAAACTGGTGTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGC 987 704 ACGGACGACGCGCGCGCGGGAACTGGGGGCTCCTGGACGCTCTGGGC 763	TGGGTGCAGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTCGGC 	Grere Gerere	884 ITCCATCGGGCCATTCCCAGAGTGGCACCGCGTTATTCAGACTTTTCATCACTGTAAC 943 	944 CCACTGAAAGTGGCCAAGAAGGTTGCCCACCTGGCTGGATGCAACACACAACAGCACACAG 1003 	1004 ATCCTGGTAAACTGCCTGAGGCACTATCAGGGACGAAGGTGATGCGTGTGTCCAACAAG 1063 	1064 ATGAGATTCCTCCAACTGAACTTCCAGAGAGACCCGGAAGAGATATCTGGTCCATGAGC 1123 	1124 CCTGTGGTGGATGCTGTGGTGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAG 1183 	1184 GTTTCATCTGTGCCCTACCTTCTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCT 1243	1244 TATATCATGAAGTTCCCGCTAAACCGGCAGGCGATGAGAAAGGAAACCATCACTAAGATG 1303 	CTCTGGAGTACCCGCACCCTGTTGAATATCACCAAGGAGCAGGTACCACTTGTGGTGGAG	1364 GAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGATGGAC 1423 		TACCIGIAIGAAITIGAGCACCACGCTCGIGGAATAAICGICAAA	4	1544 CCCCGCACTGATGGGCAGACCATGGGGATGAGATGTACTTCCTCTTTGGGGGCCCCTTC 1603 1684 1683	1604 GCCACAGGCCTTTCCATGGGTAAGGAAAGGCACTTAGCCTCCAGATGATGAAATACTGG 1663		1664 GCCAACTTTGCCGCACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCAGGCTAC 1723

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224 GGTGCCTTGCACAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGGAAAA 283 	Qy 1184 GTTTCATCTGGCCTACCTTCTAGGTGTCAACAACCTGGAATTGAATTGGCTCTTGCCT 1243
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9 22000C	QY 1664 GCCAACTTTGCCCGCACAGGAAACCCCAATGATGGAATCTGCCCTGCTGGCCACGCTAC 1723
44 CGCGAGAAAGTGGTGCTGGTGTTTCTGCAGCACAGGCTCGGCATCTTGGGCTTCCTGAGC	Oy 1724 AACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGGTCAAG 1783
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SGTCTC 	Qy 1904 CCCTGGGGAGTACTAGCCATGGGGACAAGAGTTCTACCCA 1952
884 TTCCATCGGGCCATTTCCCAGAGTGGCACCGCGTTATTCAGACTTTTCATCACTAGTAAC 943	RESULT 8 US-09-999-832A-253 ; Sequence 253, Application US/0999832A
944 CCACTGAAAGTGGCCAAGAAGGTTGCCCACCTGGCTGGATGCAACCACAACAGCACACAG 1003 	; PUDIIGATION NO. US20020192706A1 ; GENERAL INFORMATION: ; APPLICANT: Ashkenazi, Avi ; APPLICANT: Baker Kevin P.
1004 ATCCTGGTAAACTGCCTGAGGGCACTATGAGGACCAAGGTGATGGGTGTGCGAGAGAG 1063 	; AFFLICANT: Botstein, David ; AFPLICANT: Desnoyers, Luc ; AFPLICANT: Eaton, Dan ; AFPLICANT: Ferrara, Napoleon
1064 ATGAGATTCCTCCAACTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGC 1123 	; APPLICANT: Flivaroff, Ellen ; APPLICANT: Fond, Sherman ; APPLICANT: Gao, Wei-Qiang ; APPLICANT: Gerber, Hanspeter

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MIT GORDHIL RAUL COLLECTION.

MIT GLINGALL WARTH F.

ANT HILLY KENNER, COLLECTION.

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168
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
Time of Inventions Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLC7
CURRENT PELLON NUMBER: U9/09/978,189
PRIOR FILING DATE: 2001-10-15
PRIOR PELLON NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-03
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Gao, Wel-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kuljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Publication No. US20030004102A1
GENERAL INFORMATION:
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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APPLICANT: Eaton, Dan
APPLICANT: Farrara, Napoleon
APPLICANT: Farrara, Napoleon
APPLICANT: Fong, Sherman
APPLICANT: Fong, Wei-Qiang
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APPLICANT: Gartitsen, Mary E.
APPLICANT: Gaddard, Audrey
APPLICANT: Grimaldi, J. Christ
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APPLICANT: Hillan, Kenneth J
APPLICANT: Kliavin, Ivar J.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, David L.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timethy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C2.
CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 253
LENGTH: 2456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1013; DB 10;
Pred. No. 2.7e-292;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404 GATGCTACCACCTACCGCCTG---------
                                                                                                          Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey,
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hilan, Kenneth J
Kljavin, Ivar J.
Kljavin, Ivar J.
Napier, Mary A.
Pan, James;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.1%;
78.2%;
                                 Ferrara, Napoleon
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 78.2
Matches 1446; Conservative
                                                                         Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-978-608A-253
                  Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344
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                      1288 AICCIGGIAAACIGCCIGAGGGCACIAICAGGGACCAAGGIGAIGCGIGICCCAACAAG 1347
                                                                                                                                                                                                                                                                                                               1244 TATATCATGAAGTTCCCGCTAAACCGGCAGGCGATGAGAAAGGAAACCATCACTAAGATG 1303
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  ATCCTGGTAAACTGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAG
                                                                                                                                                                               1468 GTTTCATCTGTGCCCTACCTTCTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAATICTAAGGGTGGCTATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCCATCCAGG
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                                                                                                ATGAGATTCCTCCAACTGAACTTCCAGAGAGCCCGGAAGAGATTATCTGGTCCATGAGC
                                                                                                                                                                                                                                   GITICATCIGIGCCCIACCTICIAGGIGICAACAACCTGGAATICAATIGGCTTGCCT
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US-09-978-608A-253
/ Sequence 253, Application US/09978608A
/ Sequence 253, Application US/09978608A
/ GENERAL INFORMATION:
/ APPLICANT: ASTREMAZI, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David

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524 AACGIGIACGCGCCGCGCGCGCGCCCGGGGAICCCCAGCAGCAGTGGICIGGITC AACGTGTACGCGCCGGCGCGCGCCCCGGGATCCCCAGCTGCCAGTGATGGTCTGGTTC

808

Db 1684	RESULT 11 US-09-978-585A-253 US-09-978-585A-253 US-09-978-585A-253 Sequence 253, Application US/09978585A PUDIICATION NO. US20030049633A1 GENERAL INFORMATION: APPLICANT: Bater Kevin P. APPLICANT: Betrer Kevin P. APPLICANT: Betrer, Dan Dan Denoyers, Luc APPLICANT: Faton, Dan Dan Denoyers, Luc APPLICANT: Ferrara, Napoleon APPLICANT: Fong, Sherman APPLICANT: Fong, Sherman APPLICANT: Gerper, Hanspeter APPLICANT: Gerper, Hanspeter APPLICANT: Gerper, Mary E. APPLICANT: Godowski, Paul J. APPLICANT: Grimaldi, J. Christopher APPLICANT: Grimaldi, J. Christopher APPLICANT: Grimaldi, J. Christopher APPLICANT: Grimaldi, J. Christopher APPLICANT: Hillan, Kenneth J. APPLICANT: Klavin, Ivar J. APPLICANT: Klavin, Ivar J. APPLICANT: Napier, Mary A. APPLICANT: Napier, Mary A. APPLICANT: Napier, Mary A.	APPLICANT: Paoni, Valles; APPLICANT: Paoni, Valles; APPLICANT: Shelton, David L. APPLICANT: Stewart, Timochy A. APPLICANT: Stewart, Timochy A. APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: William I. TITLE OF INVENTION: Screted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERRNCE: P2630PLIS CURRENT FILIAGD DATE: 2001-10-16 NUMBER OF SEQ ID NOS: 624 Prior Application removed - See File Wrapper or Palm SEQ ID NO 253 LENGTH: 2456 TYPE: DNA ORGANISM: Homo sapiens	Ouery Match Query Match Query Match Best Local Similarity 78.2%; Pred. No. 2.76-292; Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3; Qy 224 GGTGCCTTGCAAGAGGCTCTAAGAGTGGATCACAAATATGGAACCTGCAAGAAAA 283
	1168 TTCCATGGGGCCATTTCCCAGAGTGGCACCGCGTTATTCAGACTTTTCATCACTAGTAAC 943	TATELLE ISANGE I COCCOCTANDO COSCUSSIONES CANDES AND CONTROLL IN THE ITEM IN THE CALL IN THE ITEM IS A CONTROLL IN THE ITEM IN THE ITEM IS A CONTROLL IN THE ITEM IS A CONTROL	1544 CCCCGCACTGATGGGCAGACCATGGGGATGAGTGTACTTCCTCTTTGGGGGCCCCTTC 1603 1684

1998-04-09

1998-04-15

1998-04-22

1998-04-28

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RELING DATE: 1998-04-08
APPLICATION NUMBER: 60/081049
RILLING DATE: 1998-04-08
APPLICATION NUMBER: 60/081071
RILLING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195
RILLING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
RILLING DATE: 1998-04-09
RILLING DATE: 1998-04-09
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R FILING DATE: 1998-04-29
A APPLICATION NUMBER: 60/083500
R FILING DATE: 1998-04-29
A APPLICATION NUMBER: 60/083742
R FILING DATE: 1998-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081817
FILING DATE: 1998-04-15
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
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FILING DATE: 1998-04-23
APPLICATION NUMBER: 60/083336
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083554
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APPLICATION NUMBER: 60/083558
FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/082568
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PLICATION NUMBER: 60/082569
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APPLICATION NUMBER: 60/083322
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FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/083499
FILING DATE: 1998-04-29
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FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/084414
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APPLICATION NUMBER: 60/082804
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APPLICATION NUMBER: 60/083496
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PLICATION NUMBER: 60/084441
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                                                                     APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630Pld
CURRENT APPLICATION NUMBER: US/09/976,191A
CURRENT PRING DATE: 2001-10-15
PRIOR FILING DATE: 1997-110-17
PRIOR APPLICATION NUMBER: 60/062260
PRIOR APPLICATION NUMBER: 60/062249
PRIOR APPLICATION NUMBER: 60/06231
PRIOR PLING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
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R PAPLICATION NUMBER: 60/078939

R PILING DATE: 1998-03-20

R APPLICATION NUMBER: 60/079294

R FILING DATE: 1998-03-25

R APPLICATION NUMBER: 60/079656

R FILING DATE: 1998-03-26
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R APPLICATION NUMBER: 60/079663
R FILING DATE: 1998-03-27
R PILING DATE: 1998-03-27
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079786
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R APPLICATION NUMBER: 60/080107
R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080165
R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
FILING DATE: 1998-03-11
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079689
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APPLICATION NUMBER: 60/078886
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APPLICATION NUMBER: 60/079920
FILING DATE: 1998-03-30
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PPLICATION NUMBER: 60/080327
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APPLICATION NUMBER: 60/080333
                          Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Paoni, Nicholas F.
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PRIOR APPLICATION NUMBER: 60/084640 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084598	PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084600 PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION VUMBER: 60/084627 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084643 PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/085339 PRIOR FILING DATE: 1938-05-13 PRIOR APPLICATION NUMBER: 60/085338 PRIOR FILING DATE: 1998-05-13	PRIOR APPLICATION VUMBER: 60/085323 PRIOR FILING DATE: 1998-05-13 PRIOR APPLICATION VUMBER: 60/085582 PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/085700 PRIOR FILING DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085689 PRIOR PILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/085579 PRIOR PILING DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085580 PRIOR FILING DATE: 1998-05-15	PRIOR APPLICATION NUMBER: 60/0855/3 PRIOR PILING DATE: 1998-05-15 PRIOR PLING DATE: 1998-05-05-05-05-05-05-05-05-05-05-05-05-05-	51.18; SC	Fred. NO. 1 0; Mismatch NGGCCTCAAGTGC	388 GGTGCCTTGCACAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGGAAA 447 284 CAGATGCATGTGGGGAAGACCCCATCCAAGTCTTTTAAGAGTCCCCTTCTCCAGACCT 343				628 GCACGATCTCGGCTCACTGCAACCTCCGGGTTCAAGCGAGTCTCCTGCCTCAG 687	688 CCTCTGAGTGTCTGGGGGCTACAGGTGCCTGCAGGAGTCCTGGGGGCCAGCTGGCCTCGATG 747	TACGTCAGCACGCGGGAACGGTACAGGCGCTTCAGCGAGGACTGTCTGT	, 524 AACGIGIACGCCCGCCCCCCCGGGAICCCCAGCTGCCAGTGAIGGTCTGGTIC 583 808 AACGIGIACGCCCGGCGCGCGCGCGCGGGAICCCCAGCTGCTGAIGGICIGGTIC 867	584 CCGGGAGGCGCCTTCATCGTGGGGGGCTGCTTCGTACGAGGGCTCTGACTTGGCCGCC 643	rccreace

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DR APPLICATION NUMBER: 60/078886

DR FILING DATE: 1998-03-20

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DR APPLICATION NUMBER: 60/078910

DR APPLICATION NUMBER: 60/078910

DR APPLICATION NUMBER: 60/0789910

DR FILING DATE: 1998-03-20

DR FILING DATE: 1998-03-25

DR APPLICATION NUMBER: 60/079664

DR APPLICATION NUMBER: 60/079664

DR APPLICATION NUMBER: 60/079669

DR APPLICATION NUMBER: 60/079669

DR FILING DATE: 1998-03-27

DR APPLICATION NUMBER: 60/079699

DR FILING DATE: 1998-03-27

DR APPLICATION NUMBER: 60/079929

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REPLING DATE: 1998-04-01
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APPLICATION NUMBER: 60/081838
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APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082569
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PPLICATION NUMBER: 60/082704
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLOT.
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT APPLICATION NUMBER: 09/91858
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
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                                                            1784 GAGAAGAAGATGGCTTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGG 1843
                                                                                                                      1785 GAGAAGAAGATGGCTTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGG 1844
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US-09-978-403A-253
i Sequence 253, Application US/09978403A
j PUBLICAND No. US20030050240A1
i APPLICANT: AShkenazi, Avi
j APPLICANT: Baker Kevin P.
j APPLICANT: Botstein, David
j APPLICANT: Bestein, David
j APPLICANT: Beston, Dan
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Gerritsen, Mary E.
Geddard, Audrey
Goddard, Audrey
Goddard, Autrey
Grimaldi, J. Christopher
Grimaldi, J. Christopher
Hillan, Kenneth J.
Kijavin, Ivar J.
Kujavin, Ivar J.
Kujavin, Ivar J.
Kujavin, Nary A.
Paper, Mary A.
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Shewart, Timothy A.
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R APPLICATION NUMBER: 60/077450
R FILING DATE: 1998-03-10
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R APPLICATION NUMBER: 60/077632
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APPLICATION NUMBER: 60/077649
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FILING DATE: 1998-03-12
APPLICATION NUMBER: 60/078004
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijaun, Kenneth J.
APPLICANT: Kijaun, Ivar J.
APPLICANT: Koopiaa.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Shalton, David L.
APPLICANT: Shalton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLC2A;
CURRENT APPLICANION NUMBER: US/09/978,564A
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PRIOR APPLICATION NUMBER: 60/06220
PRIOR FILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06439
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06364
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-11
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PRI
               J. Christopher
               Grimaldi,
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1408 CCTGTGGTGGATGGTGTGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAG 1467
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Publication No. US20030050241A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Brivaroff, Ellen
APPLICANT: Frivaroff, Ellen
APPLICANT: Forg, Sherman
APPLICANT: Forg, Sherman
APPLICANT: Gerber, Hanspeter
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REFLING DATE: 1998-04-15

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RAPLICATION NUMBER: 60/08269

RAPLICATION NUMBER: 60/082704

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RAPLICATION NUMBER: 60/082707

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RAPLICATION NUMBER: 60/083495

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R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081071
R FILING DATE: 1998-04-08 LING DATE: 1998-04-08
PLICATION NUMBER: 60/081203
LING DATE: 1998-04-09 LICATION NUMBER: 60/081195 60/080194 1998-04-30 LING DATE: 1998-03-3: PLICATION NUMBER: 60, PRIOR

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PRIOR APPLICATION NUMBER: 60/08441

PRIOR PILING DATE: 1998-05-07

PRIOR PILING DATE: 1998-05-07

PRIOR PELING DATE: 1998-05-07

PRIOR PLING DATE: 1998-05-13

PRIOR PLING DATE: 1998-05-15

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4,0) 0	APPLICANT: Filvaroff, Ellen APPLICANT: Filvaroff, Ellen APPLICANT: Gao, Wei-Qiang APPLICANT: Gao, Wei-Qiang APPLICANT: Gacher, Hanspeter APPLICANT: Gacher, Hanspeter APPLICANT: Gacher, Mary E. APPLICANT: Gacher, Audrey APPLICANT: Gacher, Audrey APPLICANT: Galmaldi, J. Christopher APPLICANT: Gurney, Austin L. APPLICANT: Hillan, Kenneth J APPLICANT: Hillan, Kenneth J APPLICANT: Hillan, Kenneth J APPLICANT: Napier, Mary A. APPLICANT: Napier, Mary A. APPLICANT: Roy, Margaret Ann APPLICANT: Stewart, Timothy A. APPLICANT: Bood, William; P. Mickey APPLICANT: Wood, William; P. Mickey APPLICANT: NOW, William; Colosoperate A. APPLICANT: MOSTER: 1997-11-13 PRIOR PILING DATE: 1997-11-13 PRIOR PILING DATE: 1997-11-12 PRIOR PILING DATE: 1997-11-21 PRIOR PILING DATE: 1999-1316 PRIOR PILING DATE: 1999-1316 PRIOR PILING DATE: 1999-1316 PRIOR PILING DATE: 1999-11-21
008 AACGTGTACGCGCGGCGCGCGCGGGGGATCCCCAGTGATGGTCGTTC 867	TGAGC TGAGA TG

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PRIOR PILING DATE: 1998-05-07
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1183 GTTTCATCTGTGCCCTACCTTCTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCT 1243 CCTGTGGTGGATGGTGTGGTGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAG 1467 TATATCATGAAGTTCCCGCTAAACCGGCAGGCGATGAGAAAGGAAACCATCACTAAGATG 1303 1843 1484 GCCGGCCTCCCTGTCTACCTGTATGAATTTGAGCACCACGCTCGTGGAATAATCGTCAAA 1543 1544 CCCCGCACTGATGGGGCAGACCATGGGGATGAGATGTACTTCCTCTTTTGGGGGCCCCTTC 1603 1348 ATGAGATTCCTCCAACTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGC -----AATATCACCAAGGAGCAGGTACCACTTGTGTGGTGGAG GAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGATGGTGGAC ATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCACTACCACCGAGAT GAGAAGAAGAAGACTITTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGG 1304 CTCTGGAGTACCCGCACCCTGTTGAATATCACCAAGGAGCAGGTACCACTTGTGGTGGAG GAGTACCTGGACAATGTCAATGACTTGGAAGATGCTACGAAACCGTATGATGGAC ATAGTTCAAGATGCCACTTTCGTGTATAGCCACACTGCAGACTGCTCACTACCACCCGA---AACAAGGATGAAAAGTACCTGCAGCTGGATTTTTACCACAAGAGTGGGCATGAAGCTCAAG AACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAG GAGAAGAAGACTITITGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGG CAATTCTAAGGGTGGCTATGCAGGAAGGAGCCAAAGAGGGGGTTTGCCCCCACCATCCAGG 1604 GCCACAGGCCTTTCCATGGGTAAGGAGAAGCACTTAGCCTCCAGATGATGATAATACTGG GCCAACTTTGCCCGCACAGGAAACCCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTAC CCCTGGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTTCTACCCA 1952 Page

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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
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	% Query Match Length DB	2356	3431	986	1047
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	Result No.	1	2	m	4

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramedrau, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length bonA libraries for rapid discovery of new 9 Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL MEDLINE PUBMED

TITLE

AKO37191 AKO371	BQ269800 BQ26980 BI460262 BI46026 AW512144 AW51214 CF111083 AK078879 AK0788	BB630313 AA450272 AA450272 CF116765 CF11676 BX488287 BX488287	A1949486 BX336837 BF126303 AY41459 RX397287	CF111142 CF111142 CF1111142 CF1111143 R85476 R85476 AY414461 AY414461 BG9993190 BG99931	10 BC236748 BF236748 602028044 11 AK033563 Mus muscu 11 AK03563 AK03748 Mus muscu 11 BC015286 Mus muscu 12 B1761231 BC015286 Mus muscu 11 AK078953 AK078953 Mus muscu 11 AK078953 AK078953 Mus muscu 11 AK078953 Mus muscu	AA33998 AA33939 BG013590 AA33939 BG013590 BG0135 AA865634 AA86563 BG019926 BG0189 BG019926 N44535 BE831841 BE6318	CB468793 CB468793 CB468793 BQ900930 N25091 N25091 N25091 N25091 Y BQ900803 CB464960 BU164315 CB450706 CB450706 CB450706	ALIGNMENTS 2356 bp mRNA, linear HTC 19-SEP-200 ys neonate skin cDNA, RIKEN full-length enriched 3007M20 product:hypothetical Carboxylesterases protein, full insert sequence. 085654 se mouse)
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 74 Row: d Column: 22 This clone has the following problem: retained intron. Location/Qualifiers

FEATURES

1. 3431
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mol_type="mRNA"
db_xref="taxon:9606"
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Score 900.4; DB 11; Length 3431; Pred. No. 2.9e-200; 0; Mismatches 1; Indels 0; Query Match
Best Local Similarity 99.9%;
Matches 901; Conservative (

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1851 AAGGGTGGCTATGCAGGAAGGAGCCA 1876 GAGAGTGACCAAGCAAGAGGGAGCTA 1809

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21.7 665 CGCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCCCGGGAGGCGCCTTCATCGTGG 158 909 8 P

04-MAR-2003

3431 bp mRNA linear HTC 1 HOMO sapiens, Similar to cDNA sequence BC026374, clone INAGE:2267757, mRNA.
BC041823
BC041823.1 GI:27693665

457 845 CCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTCGGCCAGTCGGCGGGGCCATGAGCA CCTTCGGGGGGGAGACCCAGGAAATGTGACCCTGTTCGGCCAGTCGGCGGGGGGCCATGAGCA 786 398 g ò

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3431)

Strausberg, R.

REFERENCE AUTHORS TITLE JOURNAL

Homo sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Homo sapiens

Direct Submission
Submitted (13-DEC-2002) National Institutes of Health, Mammalian
Submitted (13-DEC-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: agapba: "Gmall. nih.gov
Tissue Procurement: miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shirak

REMARK

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ORIGIN

/note="Vector: pBluescript"

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

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AGENCOURT 6499466 NIH_MGC_124 Homo sapiens cDNA clone INAGE:5730013 5', mRNA sequence.
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EMT. Homo sapiens (human)
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// mol_type="mRNA"

// db_xref="txxxon:9606"

// clone="txpe="natural killer cells, cell line"

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// lab host="MIH MGC 106"

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B. 1 (bases 1 to 988)

B. 1 (bases 1 to 988)

S. NIH-MGC http://mgc.nci.nih.gov/.

L. Ungublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Daniel McVicar, DBS/NCI

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llhi.gov

Plate: LLCM2121 row: Column: 14

High quality sequence stop: 675.
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AGENCOURT 6821751 NIH_MGC_106 Homo sapiens CDNA clone IMAGE:5934661
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BQ053090
TCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGGTGA 1145
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us-10-001-227-1.rst

Db 498 AGATCCTGGTAAACTGCCTGAGGGCACTATCAGG Qy 1062 AGATGCTCCCAACTGAGGGCACTATCAGGA Db 558 AGATGAGATTCCTCCAACTGAACTTCCAGAGAGA Qy 1122 GCCTGTGGTGATGGTGGTGATTCCTCCAGATGA Qy 1122 GCCTGTGGTGGATGGTGGTGATCCCAGATGA Db 618 GCCTGTGGTGGTGGTGATCCTCAGATGA Qy 1182 AGGTTTCATCTGTGCCTACTTCTAGGTGTCAA Db 678 AGGTTTCATCTGTGCCCTACTTCTAGGTGTCAA Db 678 AGGTTTCATCTGTGCCCTACCTTCTAGGTGTCAA	Oy 1242 CITAIATCATGAAGTICCCGCTAAACGGCAGG-GG-(DD 738 CITAIATCCTGAAGTICCCGCTAAACGGCAGGCQQQQQQQQQQQQQQQQQQQQQQQ	RESULT 5 BQ269800 LOCUS DEFINITION 1x30c07.x1 HR85 islet Homo sapiens claimilar to SW:ES10_RAT P16303 LIVER (i, mRNA sequence.) ACCESSION BQ269800.1 GI:20494866 KEYWORDS EST. VERYORDS FOR SAPIENS (human) OURGANISM Homo sapiens	Bukaryota, Metazoa, Chordata, Crantal Mammalia, Butheria, Primates, Catari) REFERENCE 1 (Dases 1 to 593) AUTHORS Melton, D., Brown, J., Kenty, G., Permul Tomishya, T. Crosaria M. Brestalli	Hillier, D., Marra, M., Pape, D., Wile Schmitt, A., Theising, B., Ritter, E., I Cardenas, M., Gibbons, M., Wodann, R., William, G., Cardenas, M., Gibbons, M., Wand Cann, R., William, G., Cardenas, M., Gibbons, M., Wand Cann, R.,	TITLE FACOCINE PANCESS CONSCITURM JOURNAL Unpublished (2000) COMMENT Contact: Douglas Melton, Klaus H. Ka	Harvard University, Howard Hughes Mee Dept of Molecular and Cellular Biolog MA 02138	1e1: 01-495-8557 Fax: 617-495-8557 Email: dmelton@biohp.harvard.edu Library was constructed by Dr. Hirosi	nashington university deforme organization obtaining a clone please contact; Dr (hinoue@im.wustl.edu) Possible reversed clone: similarity ear naimer. eversed clone; Similarity ear naimer.	High quality sequence stop: 439. FEATURES Location/Qualifiers 1. 593	/mol_type="mRNR" /db_xref="taxon:9666" /clone="MRMGB:6782885" /+iesue_tymo="burified mange	/lab host="DH10s" /clone lib="HR85 islet" /note="Organ: Pancreas; Vec	NOL1; Site z. Knol; CUNA ma Size-selected on agarose ge
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Bases 1 to 1047) AUTHORS NIH-MGC http://mgc.noi.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL CONTACT: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Invitrogen CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:		/ussue_type="nappocampus". /lab_host="nappocampus". /clone_lib="NIH_MGC_124" /note="Organ: brain; vector: pCMV-SPORT6; Site_1: EcoRV /note="Organ: brain; vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: Not1; RMS source male hippocampus, age_27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code_012."	Query Match 38.4%; Score 761.2; DB 12; Length 1047; Best Local Similarity 96.5%; Pred. No. 7.9e-168; Matches 789; Conservative 0; Mismatches 28; Indels 1; Gaps 1;	Oy 522 TGAACGTGTACGCGCGCGCGCGCCCCGGGGATCCCCAGTGCCAGTGATGGTCGGG 581	OY 582 TCCCGGGAGGCGCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGCTCTGACTTGGCCG 641	Oy 642 CCCGCGAGAAAGTGGTGCTGGTTTTCTGCAGAGGCTCGGCATCTTCGGCTTCCTGA 701	Oy 702 GCACGACGACGACGACGCGCGGGAACTGGGGGCTGCTGGAGATGGCGGCTCTGC 761	OY 762 GCTGGGTGCAGGAACATCGCAGCCTTCGGGGAACCCAGGAAATGTGACCCTGTTCG 821	0y 822 GCCAGTCGGCGGGGCCATGAGCATCTCAGGACTGATGATGTCACCCCTAGCCTCGGGTC 881	OY 882 TCTTCCATCGGGCCATTTCCCAGAGTGGCACGCGTTATTCAGACTTTCATCACTAGTA 941	QY 942 ACCCACTGAAAGTGGCCAAGAAGGTTGCCCACTGGATGCAACCACAACAACAC 1001 Db 438 ACCCACTGAAAGTGGCCAAGAAGGTTGCCCACTGGCTGGATGCAACAACAACAACAACAACAACAACAACAACAACAACAA	QY 1002 AGATCCTGGTAAACTGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACA 1061

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ector: pBluescript SK(-); Site_l:
made by oligo-dT priming.
gel. Average insert size ~1kb. 5'
                                                     AACCCGGAAGAGATTATCTGGTCCATGA 1121
                                                                                                                       ACCCTTTGGTGCTCCTGACCCAGGGGA 1181
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SGACCAAGGTGATGCGTGTGCCAACA 557
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i, J., Gradwohl, G., Clifton, S.,
lile, T., Martin, J., Blistain, A.,
I., Ronko, I., Bennett, J.,
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Best Local
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AW512144
LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           526 bp mRNA linear EST 21-AUG-2001
G03201884F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5267757 5',
B1460262
Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permut Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692.
                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                            432 TGCAGGAGTCCTGGGGCCAGCTGGCCTCGATGTACGTCAGCACGCGGGAACGGTACAAGT 491
                                                                                                                                                                                                                                       551
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Email: agapbs-r@mail.nih.gov
Tisaue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 526)
NIH (Masses 1 to 726)
NIH "MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                     GGGATCCCCAGCTGCCAGTGTCTGGTTCCCGGGAGGCGCCTTCATCGTGGGCGCTG
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0
                                                                                                                    DB 13; Length 593;
                                                                                                                                                Indels
                                                                                                                                                   1;
                                                                                                                 Score 591.4; DB 13.
Pred. No. 4.9e-128;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI460262.1 GI:15250918
                                                                                                                    29.8%; al Similarity 99.8%; 592; Conservative
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Homo sapiens
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                                                                                                                  Query Match
Best Local S:
Matches 592
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Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information of found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLANI1675 row, g column: 22
High quality sequence stop: 525.
High quality sequence stop: 525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.3%; Score 482.4; DB 12; Length 99.8%; Pred. No. 2e-102; ive 0; Mismatches 1; Indels
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Gaps
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                                            851 GGACTGATGATCACCCTTAGCCTCGGGTCTTCCATCGGGCCATTTCC 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.2%; Score 401.4; DB 14; Length 1918;
larity 55.7%; Pred. No. 5.1e-83;
Conservative 0; Mismatches 651; Indels 12;
                                                              /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="Contig3845"
                                                                                                                                                                                                                                     CF111083.1 GI:33167595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .1918
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Matches 834;
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CF111083
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DEFINITION
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                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Libra at:
image.llnl.gov/image/html/iresources.shtml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NCI_CGAP_Ut1"
/clone_lib="NCI_CGAP_Ut1"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
similar to SW:ES10_RAT P16303 LIVER CARBOXYLESTERASE 10 PRECURSOR; mRNA sequence.
                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 468)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTGCAGGAGTCCTGGGCCTGGGCTCGATGTACGTCAGCACGCGGGAACGGTACAAG
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="reaxon:9606"
/clone="IMAGE:2805548"
/tissue_type="well-differentiated endometrial
/lab_host="DH108"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Possible reversed clone: similarity on wrong strand Seg primer: -40UP from Gibco High quality sequence stop: 406. Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Indels
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Pred. No. 7.9e-91;
0; Mismatches 9;
                                                 AW512144.1 GI:7150222
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ilarity 97.5%;
Conservative C
                                                                                      Homo sapiens (human)
Homo sapiens
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Best Local 8
                                                     VERSION
KEYWORDS
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AUTHORS
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Rattus.

1 (Dasses 1 to 1918)

Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V.,
Padua,A.M., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B.,
Plopper,C.G. and Buckpitt,A.R.
Gene Expression Analysis in Response to Lung Toxicants: I.
Gene Expression Analysis in Response to Lung Toxicants: I.
Gene Expression Analysis of Response to Lung Toxicants: I.
Gene Expression Analysis of Response to Lung Toxicants: I.
Gene Expression Analysis of Response to Lung Toxicants: I.
Contact: Shultz MA
Dept. of Molecular Biosciences, School of Veterinary Medicine
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1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
Tel: 530 752 4698
Email: mashultr@wucdavis.edu
Aversge Phred score is 20 or better. All poor quality data (Fhred < 20) and vector/linker sequence has been removed.
High quality sequence stop:
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/dev_stage="adult"
/clone_lib="Rat lung airway and parenchyma cDNA libraries"
/note="Organ: lung, Vector: pGEW-112f(-); Site_1: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
lung_airways and parenchyma tissues."
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361 CGGGGGGGGCCANGAAATGTGACCCTGTTCGGCCAGTCGGCGGGGGCCATGAGCATCTCA 420
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Sattus norvegicus (Abradata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Qy 1628 GAGAAGGCACTTAGCCTCCAC Db 1490 GAGACCAATCTAGCAAAATC Qy 1688 CCCAATGATGGGAATCTGCCC Db 1550 CCTAATGGGGAAGGTTGCCC Qy 1748 CTGGATTTACCACAAGAGTC Qy 1748 CTGGATTTACCACAAGAGTC Db 1610 ATTGGTGCCTCAACTCAGGGCA	RESULT 9 AK078879 LOCUS DEFINITION MUS musculus adult male library, clone:9030604P sequence. ACCESSION AK078879.1 GI:26347580 KEYWORDS HTC; CAP trapper. SOUNCE MUS musculus (house mou	BURATYOL3, MELEZOA; Cho REFERENCE 1 AUTHORS Carninci, P. and Hayashi TITLE High-efficiency full-le JOURNAL MECH. Enzymol. 303, 19- MEDLINE 99279253 PUBMED 10349636 REFERENCE 2 AUTHORS CARNINCI, P., Shibata, Y. TITLE NORMELLINE SHE	SHEER	Yamamoto, R., Matsumoto, Fujiwake, S., Inoue, K., Yoneda, Y., Inbikawa, T., Okazaki, Y., Muramatsu, M. TITLE RIKEN integrated sequen sequencing pipeline with MEDLINE 20530913 PUBMED 11076861	വ പലശ	JOURNAL Nature 420, 563-573 (200) REFERENCE 6 (bases 1 to 1944) AUTHORS Adachi,J., Alzawa,K., Hayatsu,N., Hayatsu,N., Hayatsu,N., Hayatsu,N., Hayatsu,N., Hayatsu,N., Hayatsu,N., Kawai,J., Koja,K., Kawai,J., Koja,K., Kawai,J., Koja,K., Nakamura,K., Naka
	731 TGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGCAGAGAACATCGCAGCCTTC 790	911 ACCGCGTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGGTTGCC 970 776 GTGTCCTCAATACTGCTCTCAATACAACAGATAGCAAGCCCATTGCTAATCTGATTGCT 835 971 CACCTGGCTGGATGCAACCACAACAGATCCTGGTAAACTGCTGAGGGCACTA 1030 836 ACTCTTTCTGGGTGTAAAACCACCACACAGATCGTTTATGGTTCATTGCCTGCGCCAGAAG 895 1031 TCAGGGGACCAAGGTGATGCGTGTCCAACAAATTGAATTCTCCCAACTCCAACTCCAG 1090 104 TCAGGGACCAAGGTGATGCGTGTCCAACAAAATTGAATTCTTCCAACTCAAACTCCAACAATTCAACTCTAAAATTGAATTCTTTAAAATTCAACTCAAACTCCAACAAATTGAATTTAAAATTCAAACTTCAAATTTAAAATTCAAACTTCAAATTTAAAATTTAAAATTTAAAATTTAAAATTTAAAATTTAAAA	AGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGTGGTGGTGGTGCGTCCA 11	1211 GTCAACAACCTGGAATTCAATTGGCTCTTATATCATGAAGTTCCGGTAAACCGG 1270	ACTCTGAGAAATGATTCCAATGGCTTCTGAGAAGTATTTAGGAGGACAGATGACCCT GACTGGAAGATGCTACGAATGGCTTCTGAGAAGTATTTAGGAGGACAGATGACCCT GACTGGAAAGATGCTACGAATGATGATGATCAAGATGCCACTTTCGTGTAT	1310 CCATCAGTGATGATGTCTCGAAGTCACAGAGATGCTGGAGCCCCCACCTTCATGTATGAA 1369 1511 TTTGAGCACCACGCTCGTGGAATAATGGTCAAACCCGCACTGATGGGGCCACACCAT 1567 1370 TTTGAGTATCGCCCAAGCTTTGTATCAGCCATGAGGCCCAAGACACATGATCGCACAGACCAT 1429 1568 GGGGATGAGATGTACTTCCTCTTTGGGGCCCCTTCGCCACAGGCCTTTCCATGGGTAAG 1627 1568 GGGGATGAGATGTACTTCCTCTTTTGGGGCCCCTTCGCCACAGGCCTTTCCATGGGTAAG 1627 1430 GGTGATGAAATCTTCTCAGTATTTGAAAGATGGCGCTCAGAAGAG 1489
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Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Nakamura,S., Hazama,M.,
Nishine,T., Harada,A.,
Oto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
T., Ozawa,K., Tanaka,M., Ohara,E., Watahiki,M.,
T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Su,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
Wuth 384 multicapillary sequencer
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AGATGATGAAATACTGGGCCAACTTTGCCCGCACAGGAAC 1687
                                                                                                                                                                                     CCTGCTGGCCACGCTACAAGGATGAAAAGTACCTGCAG 1747
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raaki,Y., Muramatsu,M. and Hayashizaki,Y.
raction of cap-trapper-selected cDNAs to
the libraries for rapid discovery of new genes
(617-1630 (2000)
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Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagawi, M., Tagawa, A., Takahashi, F., Takaku-Akahira, Sogabe, Y., Tanaka, T., Tomaru, A., Tayawa, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Toya, T., Yasunishi, A., Direct Submission

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, VR.:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216 Center and Sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
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/clone lib="RIKEN full-length enriched mouse cDNA library"
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
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Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
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Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
GAGAAGGCACTTAGCCTCCAGATGAAATACTGGGCCAACTTTGCCCGCACAGGAAAC 1687
                                                                                                                          1522 GAGACCAACCTCAGCAAGATGGTGATGAATTCTGGGCCAACTTTGCTCGGAATGGGAAC 1581
                                                                                                                                                                            CCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAAGAAGATGAAAGTACCTGCAG 1747
                                                                                                                                                                                                         BB630313 RIKEN full-length enriched, 6 days neonate skin Mus musculus cDNA clone A030007M20 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                    1642 ATTGGTGCCTCAACTCAGGCACCCCAGAGGCTGAAGGACAAAGAAGTGAGTTTTTGG 1698
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                               1748 CTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTGG
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/note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was GAGAGAGAGAGCTCTTTTTTTTTTTTTTVN 3'1, cDNA was
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Pred. No. 2.6e-76;
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Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
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Best Local Similarity 84.1%; Pred. No. 1.7e-70;
Matches 391; Conservative 0; Mismatches 74; Indels 0;
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Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora;

Bovidae; Captinae; Ovis.

1 (bases 1 to 478)

DeSilva, U., Franklin, I.R., Maddox, J.F., van Hest, B. and

Adelson, D.L.

Gene Expression in Sheep Skin and Wool (Hair)

Cytogenet. Genome Res. (2003) In press

Animal Breeding and Genetics
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Fax: 9798456970
Email: david.adelson@tamu.edu.
Location/Qualifiers
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Eukaryota; Matazoa; Chordata; Catarrhini; Hominidae; Homo.
El (Sases Ito 403)
El (Sases Ito 403)
El Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Morte, El, Schellenberg, K., Steptoe, M., Tan, P., Theising, B., Washute, Y., Wylie, T., Waterston, R. and Wilson, R., Theising, B., Washu-Merck EST Project 1997
L Dupublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGAAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGGTGATCCCAGATGACC 1157
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                                                                                                                        EST 04-JUN-1997
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                                                                                         AM43U272

ZX42N02.r1 Soares total fetus Nb2HFB 9w Homo sapiens cDNA clone
IMAGE:789171 5' sTmilar to TR:G1931 G1931 CARBOXYLESTERASE
PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
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Pred. No. 1.4e-74;
0; Mismatches 7; Indels 2.
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97.7%;
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DKFZp686E07269_r1 686 (synonym: hlcc3) Homo saplens cDNA clone
DKFZp68E07269<sup>-5</sup>', mRNA sequence.
BX48B287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 442)
Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
EST (Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., et al.) Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DRZ); Email s.wiemannedkfz- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl. sequence available.
This clone (DRZD686E07266) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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GGTGCCTGCAGGAGTCCTGGGGCCAGCTGGCCTCGATGTACGTCAGCACGCGGGAACGGT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Site_1: SfiIA; Site_2: SfiIB;
                                                       194 TAAATGGCTGCACTTCAATGAGGACTGTCTGTACCTGAATGTGCACGCGCCAGTGCGAGC
                                                                                                         GCCCGGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCCCGGGAGGCGCCTTCATCGTGGG
                                                                                                                                         254 GCGCGGGGACCTTCTGCAGCCCGTGATGATCTGGTTCCCAGGAGGCGCCTTCCTCGTGGG
                                                                                                                                                                                                              314 TICCGCTICCACGIACGAIGGCTCCGAATIGGCTGCCCGGGAGAAGTGGTGGTCGTGGT
                                                                                                                                                                                                                                                  CGCTGCTTCTTCGTACGAGGCTCTGACTTGGCCGCCCGCGAGAAGTGGTGCTGGTGTT
                                  GGTGCCTGCAGGAGTCCTGGGGCCAGCTGGCCTCGATGTACGTCAGCACGCGGAACGGT
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Similarity 100.0%; Pred. No. 1.1e-69;
13; Conservative 0; Mismatches 0;
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/lab_host="DH10B"
/clone_lib="686 (synonym: hi/note="Vector: priplEx2; S; cDNA-collection"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686E07269"
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MIPS
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Best Local Simi
Matches 343;
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BX488287
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/organism="Homo sapiens"
//organism="Momo sapiens"
// Mol type="mRNN"
// Ab_Fref="taxon:9606"
// Johne="Thast." Apple: 10903"
// Lissue_type="2 pooled tumors (clear cell type)"
// Johnest="Dhilds"
// Johnest="Mol CGAP Kid12"
// Johnest="Mol CGAP Kid12"
// Johnest="Mol CGAP Kid12"
// Johnest="Mol CGAP Kid12"
// Johnest Kidney; Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1: Site 2: Eco R1.
// Plasmid DNA from the normalized library NOT CGAP Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonelDs 1325312-1325831, 1471368-1472903 and 1422104-1493225). Subtraction by Bento Soares and M. Fatima Bonaldo.
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Email: cgapbs-remail.nih.gov

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Christopher Moskaluk, M.D., Ph.D., Michael R.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clond Aistribution: NGT-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 490 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 330.
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                                                                                                               160 ACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCTGAACGTGTACGCGCCCGGCGCG
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1836

455

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CCCCTTCGCCACAGGCCTTTCCATGGGTAAGGAGAAGGCACTTAGCCTCCAGATGATGAA 1656
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CCGAGATGCCGGCCTCCCTGTCTACCTGTATGAATTTGAGCACCACGCTCGTGGAATAAT 1536
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/ Organism=Homo sapiens"

/ Anol_type="mrMA"

/ Clone="CSC01033YE23"

/ Lissue_type="PLACENTA COT 25-NORMALIZED"

/ Clone="Ib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/ note="list strand cDNA was primed with a Not1-oligy(dT)

/ note="list strand cDNA was primed with a Not1-oligy(dT)

/ note="list strand cDNA was primed with a Not1-oligy (dT)

/ siner Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."
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1. (bases 1 to 884)
Li, W.B., Gruber, Gruber, Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                    374 ACAGGAGCTGGAGCATGAGGTGGATTCTGTGCTGGAGCCTCACCCTTTGCCTGATG
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Invitrogen. This sequence belongs to sequence cluster 8153.f.,
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrocen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI033AC12QP1.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 3, 2004, 22:23:05; Search time 57 Seconds (without alignments) 2894.873 Million cell updates/sec

US-10-001-227-2 3112 1 MPSTVLPSTULPTAGA.......KWAFWMSLYQSQRPEKQRQF 584 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
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7: geneseqp2003bs:*
8: geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	4 Human	Aae21052 Human dru	5 Novel	Human 8	2 Human	3428 Human	Abu87976 Novel hum	Abu84291 Human sec	Abr66165 Human sec	Abr65555 Human sec	95 Human	34 Human	Abu89855 Novel hum	Abr68104 Human sec	Abu96157 Novel hum	Abu92588 Human sec	Abo08665 Human sec	Abo02717 Human sec	Abr74871 Human sec	Abr94633 Human sec	Abo25225 Novel hum	Abu85606 Human PRO	Abu98766 Novel hum	Abu97981 Novel hum	Abu91687 Novel hum
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ALIGNMENTS

RESULT 1

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Carboxylesterase-2; COB-2; human; antinflammatory; virucide; antistendatic; antirheumatic; antitheumatic; dermatological; antistendatic; antitheumatic; antitheumatic; dermatological; antipsoriatic; antitheumatic; antitheumatic; dermatological; antipsoriatic; antitheumatic; antitheumatic; dermatological; compain. Key Domain Domain	X		
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Domain 3605 /note= domain" Domain 3645	F		cocaine B-esterase
/note=domain" Domain 364. 5	H	Domain	360542
domain".3645	L		II
Domain 364.	ΕŁ		domain"
	FT	Domain	. 364577

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The present sequence is the protein sequence of human carboxylesterase-2 (CDE-2), a novel carboxylesterase family member. CDB-2 participates in the metabolism of various lipid and fatty acid compounds which are involved in pain and/or inflammation signalling. It is highly expressed in tissues which contain afferent neurons, particularly brain and spinal cord tissues which contain afferent neurons, particularly brain and spinal cord tissues which contain afferent neurons, particularly brain and spinal cord tissues which contains achieved and motified a number of characteristic domains and motifis in the COE-2 amino acid sequence. The invention provides COE-2 nucleic acid molecules, antisense nucleic acid molecules, recombinant expression vectors, host cells, ransgenic animals, isolated COE-2 proteins, tusion proteins, antisense peptides and anti-COE-2 pattibodies. COE-2 binding substances are used in an inflammatory or pain disorder. Compounds capable of treating an inflammatory or pain disorder. Compounds capable of treating an inflammatory or pain disorder. Compounds capable of treating an include hyperalgesia, pain associated with musculoskeletal disorders and allergic reaction, asthma, associated with musculoskeletal disorders and include hyperalgesia, pain associated with musculoskeletal disorders and alsorder. Carboxylesterase-associated inflammatory disease, inflammatory disorders, peritonitis, short inflammatory disease, lung inflammatory astrakits, scleroderma, psoriats, inflammatory disease, inflammatory chronitis, septic offermation, polymyosociates, chronitis, chord inflammatory boxel disorders include viral inflammatory disease, inflammatory because there's syndrome, psoriatis, pellaroderma, psoriates, polymosociates, chronitis, cancer, aberrant blood clotting, misreonlation of various reproductive versat blood clotting, misreonlation of various reproductive versat plotting, misreonlatical disorders aberrant blood clotting.
                                                                note= "carboxylesterase signal serine liver glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aberrant blood clotting, misregulation of various reproductive functions e.g. induction of labour, and misregulation of the sleep/wake cycle. COE-2 nucleic acids and polypeptides are also useful in screening assays,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection assays (e.g., chromosomal mapping, tissue typing, forensic biology) and predictive medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics)
                                                                                                                                                                                                                     /note= "esterase hydrolase domain"
536. .580
/note= "carboxylesterase hydrolase precursor domain"
  note= "esterase carboxylase serine alpha esterase
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Thote= "acetylcholinesterase domain"
115. .573
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                                                                           1 MPSTVLPSTVLPSLLPTAGAGWSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQ
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100.0%; Score 3112; DB 5;
100.0%; Pred. No. 1.9e-286;
ive 0; Mismatches 0;
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                                       584; Conservative
                   Similarity
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Matches 584
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1. .43 /label= Signal_peptide Location/Qualifiers

Homo sapiens

Peptide

Sequence 584

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The invention relates to an isolated human drug metabolising enzyme (DME)

colypeptide or a biologically active or immunogenic fragment of DME. DME

catcoimmune/inflammatory, developmental, endocrine, eye, metabolic and

catcoimmune/inflammatory, developmental, endocrine, eye, metabolic and

catcoimmune/inflammatory discress including live disorders. Autoimmune/

conflammatory discress including live disorders. Autoimmune/

conflammatory discress syndrome, Addison's disease, atherosclerosis,

adult respiratory distress syndrome, Addison's disease, autoimmune

conflits, Crohn's disease, atopic dermatitis, diabetes mellitus,

conflitis, Crohn's disease, atopic dermatitis, diabetes mellitus,

conflitis, uveitis, viral, bacterial, protozoal, parasitic,

tungal, helminnic infections and trauma. Cell proliferative disorders

conflude cancer, arteriosclerosis, cirrhosis and psoriasis; developmental

disorders of hypothatemus/pituitary, disorders associated with

chypopituitarism, including diabetes insipidus, hypogonadism, disorders

conflucted with hypothyroidism including goitre, Grave's disease,

confluencials, disorders associated with gonadal steroid hormones such as

confluencials, disorders associated with gonadal steroid hormones such as

confluencials, disorders associated with gonadal steroid hormones such as

confluencials, disorders associated with gonadal steroid hormones such as

confluencials of the eye include conjunctivitis and macular degeneration and

metabolic disorders include diabetes, cystic fibrosis, obesity and

metabolic disorders include diabetes, cystic fibrosis, obesity and

confluency hepatitis, constipation, diarrhoes, jaundice, Wilson's disease,

thrombosis and hepatic tumours. DME gene is useful in gene therapy. The

constipation diarrhoes, and purchen is useful in gene therapy. The
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AK, Griffin JA, Hafalia AJA, Khan FA, Lal P. Lee S, Lu DAM;
Patterson C, Ramkumar J, Ring HS, Sanjanwala MS, Tang YT;
velu K, Thornton M, Tribouley CM, Walia NK, Warren BA, Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human drug metabolizing enzyme polypeptide and polynucleotide useful for diagnosing, treating and preventing cell proliferative, autoimmune/inflammatory, endocrine, eye, metabolic and gastrointestinal disorders.
44. .584
/note= "Mature human DME-10 protein"
137. .147
137. .247
231. .246
/note= "Carboxylesterase B1 motif"
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; 2000US-0230063P.
; 2000US-0232244P.
; 2000US-0234269P.
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2000US-0224728P.
2000US-0226440P.
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N-PSDB; AAD33489.
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Thangavelu K, T
Yao MG, Yue H;
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18-AUG-2000; 2
24-AUG-2000; 3
31-AUG-2000; 2
20-SEP-2000; 2
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Gandhi AR,
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                                                Query Match 100.0%; Score 3112; DB 5; Length 584; Best Local Similarity 100.0%; Pred. No. 1.9e-286; Matches 584; Conservative 0; Mismatches 0; Indels 0
Sequence 584 AA;
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GKQMHVGKTPIQVFLGVPFSRPPLGILRFAPPEPPEPWKGIRDATTYPFGCLQESWGQLA
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                                                                                                GKOMHVGKTPIQVFLGVPFSRPPLGILRFAPPSPPEPWKGIRDATTYPPGCLQESWGQLA
                                                                                                                                                                                                                                                                                                                                         181 AAREKVVIVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTL
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23-AUG-2000; 2000US-00649167.
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15-APR-19
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                                                                                                                                                      Homo
 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed censes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences. ABG00010-ABG30377 respected to DNA and canno acid sequences. ABG00010-ABG30377 respected to DNA and canno acid sequences. ABG00010-ABG30377 respected of but was obtained in electronic format directly from WIPO at the sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGARRCIHEFWGQLASMYVSTRERYKWLRFNEDCLYLNVYAPARAPGDPQLPVMVWFPGG
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responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                      76.8%; Score 2391.5; DB 4; Length 509; 90.9%; Pred. No. 5e-218; ive 2; Mismatches 13; Indels 31;
                                       Claim 20; SEQ ID NO 40994; 103pp; English.
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Best Local Similarity 90.9
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Human, PRO; EST; expressed sequence tag; PCR primer; hybridisation, probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
                                                                          Human PRO873 protein sequence.
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98US-0082704P.
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98US-0083392P.
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9803-0083496P.
9803-0083499P.
9803-0083500P.
9803-0083545P.
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17-MAR-1998;
20-MAR-1998;
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01-APR-1998;
01-APR-1998;
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07-DEC-1999
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29-APR-1998; 29-APR-1998;

AAY41723 ID AAY41723 standard; protein; 545 AA

RESULT 4

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226 205

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PRO polypeptide; mammal; tummour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tummour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
                                                                                                                                                                                            LOLNFORDPERIIWSMSPYVDGYVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPYIM 385
                                                                                                                                                                                                                                                                                                  386 KFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEBYLDNVNEHDWKMLRNRMDIVQ 445
                                                                                                                                                                                                                                                       266 AISQSGTALFRIFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMFF
                                                  APARAPGDPOLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD
                                                                           APARAPGDPQLPVWWWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD
                                                                                                                 SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR
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03-MAR-2000; 2000MG-US005641.
14-MAR-2000; 2000US-0189320P.
14-MAR-2000; 2000US-0189320P.
14-MAR-2000; 2000US-0189320P.
15-MAR-2000; 2000US-0190828P.
21-MAR-2000; 2000US-0191048P.
21-MAR-2000; 2000US-0191048P.
21-MAR-2000; 2000US-0191048P.
21-MAR-2000; 2000US-0191048P.
29-MAR-2000; 2000US-0191303P.
29-MAR-2000; 2000US-0191303P.
29-MAR-2000; 2000US-019444PP.
04-APR-2000; 2000US-019444PP.
04-APR-2000; 2000US-019444PP.
01-APR-2000; 2000US-019469P.
01-APR-2000; 2000US-019469P.
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98US-0083558P

98US-0083558P

98US-008436FP

98US-0084414P

98US-0084627P

98US-0084637P

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98US-0086430P
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Matches 399; Conservative
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N-PSDB; AAZ34105.
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AISQSGTALFRIFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRF 325
                                                                                                                                                                            LOLNFORDPEELIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPYIM 385
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                                                                                                          347 AISOSGTALFRIFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKWRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and to screen for modulators of the compounds.
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          18 APR-2000; 20000S-0199121P.
25 APR-2000; 20000S-0199397P.
25 APR-2000; 20000S-0199397P.
25 APR-2000; 20000S-0199550P.
25 APR-2000; 20000S-0199550P.
25 APR-2000; 20000S-0199550P.
17 AAY-2000; 20000S-0199541.
17 AAY-2000; 2000WO-US014042.
22 AAY-2000; 2000WO-US014941.
02 -UUN-2000; 2000WO-US014941.
03 -UUN-2000; 2000WO-US01564.
05 -UUN-2000; 2000WO-US029832P.
24 -AUG-2000; 2000WO-US029832P.
25 -AUG-2000; 2000WO-US039328.
26 -UUN-2000; 2000WO-US039328.
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20-DEC-2000; 2000WO-US034956
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PR 01-UUL 1998; 98 US-001654P.
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PR 13-MUC 1998; 98 US-001654P.
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PR 13-MUC 1998; 98 US-001654P.
PR 14-MUC 1998; 98 US-001654P.
PR 15-MUC 1998; 98 US-001654P.
PR 15-MUC 1998; 98 US-001654P.
PR 16-MUC 1998; 98 US-001654P.
PR 17-MUC 1998; 98 US-001654P.
PR 18-MUC 1998; 98 US-00165

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                                                                                                                                                                                          SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR
                                                                                                                                                                                                                           AISQSGTALFRIFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRF
                                                                                                                                                                     SHARGNWGLLDQMAALRWVQENIAAFGGDFGNVTLFGQSAGAMSISGLMMSPLASGLFHR
                                                               LPSTVLPSLLPTAGAGWSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMH
                                                                                                                                                             APARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD
                                                                                                                              -------CLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVY
                                                Gaps
                                                67;
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                                  Length 545,
                                                26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secreted and transmembrane protein PRO873.
                                 9
                                65.1%; Score 2026.5; DB 6; 80.3%; Pred. No. 2.8e-183; ive 5; Mismatches 26;
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98US-0103449P.
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18-SEP-1997;
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                                                                and transmembrane protein; PRO; TNP-alpha;
factor alpha; chondrocyte cell; tumour; gene therapy;
                                               Human secreted/transmembrane protein (PRO) #29.
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970S-0053266P.
970S-006344P.
970S-0063544P.
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98US-0084643P.
98US-0085579P.
98US-0085580P.
98US-0085582P.
                                                                                                                                                              2002US-00176756
                            02-AUG-2003 (first entry)
                                                                Human, secreted a tumour necrosis fitissue typing.
                                                                                                                        US2003032112-A1.
                                                                                                      Homo sapiens.
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                                                                                                                                                                                                            KFPLNRQAMRKETI TKMLMSTRTLLNI TKBQVPLVVEEYLDNVNEHDWKKLRNRMMDI VQ
                                                                                       AISQSGTALFRLFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKWRF
SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO; secreted protein; transmembrane protein;
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       98US-0096959P.
98US-0097022P.
98US-0097022P.
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98US-0097074P.
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Best Local Similarity 80.3
Matches 399; Conservative
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16-SEP-1998;
16-SEP-1998;
16-SEP-1998;
17-SEP-1998;
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                                                                                                                                                                                                                         APARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD
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                                                                                                                                                                                              LPSTVLPSLLPTAGAGWSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMH
                                                                                 Gaps
                                                                                61;
                                                             DB 6; Length 545;
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted polypeptide PRO873, SEQ ID NO:58.
                                                             65.1%; Score 2026.5; DB (80.3%; Pred. No. 2.8e-183; iive 5; Mismatches 26;
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98US-0102570P.
98US-0102571P.
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                                                               Query Match
Best Local Similarity 80.3
Matches 399; Conservative
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     Human; secreted and transmembrane protein; PRO; TNF-alpha;
tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
tissue typing.
                                                                                                                                Human secreted/transmembrane protein (PRO) #29.
                        ABU99495 standard; protein; 545 AA
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9708-0059268P.
9708-0051210P.
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                                                                                               (first entry)
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AISOSGTALFRIFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRF 325
  287 SHARGNWGLLDQWAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 346
                                                                                                                                     LQLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPYIM 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGSTSTPATTSAPSSGFGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLQGKQMH
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Best Local Similarity
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21-NOV-1997;
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27-MAR-1998;
27-MAR-1998;
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   LQLNPQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPXLLGVNNLEFNWLLPYIM 385
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                                                                                                                                                                                       APARAPGDPQLPVMVWFPGGAPIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene therapy; tissue typing; tumour; chondrocyte proliferation; chondrocyte differentiation; tumour necrosis factor-alpha release; affinity purification.
                                                                                             67;
                                                                           Length 545;
                                                                                              26; Indels
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                                                                           Score 2026.5; DB 6;
Pred. No. 2.8e-183;
5; Mismatches 26;
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80.3%; Pred
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98US-0103355P.
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Best Local Similarity 80.3
Matches 399; Conservative
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 10-JUN-1998 | 10-JUN-1998 | 11-JUN-1998 | 11
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Length Query Match
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Matches 399; Conservative 5; Mismatches 26; Indels 98US-0100664P.
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28-MAY-1998;
28-MAY-1998;
02-JUN-1998;
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Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNP-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthrits; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; civer; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
                                                                           Human secreted polypeptide PRO873, SEQ ID NO:58.
                       ABR68104 standard; protein; 545 AA
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97US-0053266P.
97US-0063121P.
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98US-0084366P.
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28-0CT-1997,
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31-0CT-1997,
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LOLNFORDPEELIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPYIM 385
                                                                                                                                                                         KFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVBEXLDNVNEHDWKWLRNRMDIVQ 445
                                                                                    AISQSGTALFRLFITSNPLKVAKKVAHLACCNHNSTQILVNCLRALSGTKVMRVSNKMRF 325
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                                                       APARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD
            SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR
                                                                                                                                                                                                                                                                                                                                                                              knockout; chromosome identification; tissue typing; tumour; chondrocyte proliferation; chondrocyte differentiation; tumour; tumor necrosis factor-alpha release stimulator.
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97US-0063250P.
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                                                                                                                                                                                                  -----CLQESWGQLASMYVSTRERXKWLRFSEDCLYLNVY
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                                                                                                                          Gaps
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                                                                                                     Query Match 65.1%; Score 2026.5; DB 6; Length 545; Best Local Similarity 80.3%; Pred. No. 2.8e-183; Matches 399; Conservative 5; Mismatches 26; Indels 67;
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29-SEP-1998;
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                                                                                                                                                                            Sequence 2, Application US/09264737A; Patent No. 6107549; CENERAL INFORMATION: FROM FAUL C.C. APPLICANT: Ruff, Thomas G. TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via TITLE OF INVENTION: Engineering Plant Resistance in TITLE OF INVENTION: Expression of Esterase Enzymes; FILE REFERENCE: 38-21(16551) RLE3 Pyridine Tolerance CURRENT APPLICATION NUMBER: US/09/264,737A; CURRENT FILING DATE: 1998-03-10
; CURRENT PELING DATE: 1998-03-10
; DARLIER FILING DATE: 1998-03-10
; SEQ ID NO S: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO S: LENGTH: 566
; TYPE: PRT
; ORGANISM: Rabbit
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Best Local Similarity 43.7%; Pred. No. 2.5e-119;
Matches 248; Conservative 117; Mismatches 175; Indels
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US-08-446-100-21
US-08-446-100-20
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US-08-347-878-34
US-08-461-8818-1
US-08-461-8818-3
US-08-461-8818-3
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                                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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LMWSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVAHLAGCNHNSTQI--LVNCLRA 310
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                                                                          EDCLYLNIYTPADLTKRGRLPVMVWIHGGGLVLGGAPMYDGVVLAAHENFTVVVVAIQYK 178
                                                                                                                                                            LGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQS--AGAMSISG 252
                                                                                                                                                                                                                                  LGIWGFFSTGDEHSRGNWGHLDQVAALHWVQENIANFGGDPGSVTIFGESFTAGGESVSV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 LSGTKVMRVSNKMRFLQLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQG--KVSSVPY 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 LIGVNNLEPNWLLPYIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLV--VEEYLD 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09140933

Padennec 2, Application US/09140933

Patent No. 602219

GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymatic Process for the Manufacture of
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of TITLE OF INVENTION: 2-Keto-L-Gulonic Acid
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 KSEDELLDLTLKMKFLTLDFHGDQRESHPFLPTVVDGVLLPKMPESILAEKDFTFNTVPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 NVNEHDWKMLRNRMMDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHH----ARGIIVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484 RTDGADHGDEMYFLFGGPFATGLSMGKEKALSLQMMKYWANFARTGNPNDGNLPCWP--R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  542 YNKDEKYLQLDFTTRVGMKLKEKKMAFWMSLYQSQRPEK 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/845,295
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APPLICATION NUMBER: US 60/017,879; 0FILING DATE: 17-May-96; 25-April-97 ATTONNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/140,933
FILING DATE: 27-August-98
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECOMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REALABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 584 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Eastman Cl
P.O. Box 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Kingspo-
STATE: Tennessee
COUNTRY: USA
ZIP: 37662-5075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALL...
STREET: F.C.
CITY: Kingsport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-140-933-2
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                                                                                                                                                            495
                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hubbe, John C.
TITLE OF INVENTION: Enzymatic Process for the Manufacture of
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of
TITLE OF INVENTION: 2-Keto-L-Gulonic Acid
TITLE OF INVENTION: 2-Keto-L-Gulonic Acid
TITLE OF ENVENTION: 2-Keto-L-Gulonic Acid
TITLE OF INVENTION: 2-Keto-L-Gulonic Ac
378 NWLLP-YIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKML 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 RPPLGILRFAPPEPPEPPEPWKGIRDATTYPPGCLQESWGQLASMYVST----RERYKWLRFS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118
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                                                                                                                                                    RNRMMDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHH-ARGIIVKPRTDGADHGDEMY
                                                                                                                                                                                                                                                                                                        FLFGGPFATGLSMGKEKALSLOMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLOLDFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 WILCWSLTLCLMAQTALGALHTKRPQVV-TKYGTLQGKQMHVG----KTPIQVFLGVPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                 | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 37.6%; Score 1169.5; DB 2; Best Local Similarity 43.0%; Pred. No. 6.9e-111; Matches 249; Conservative 108; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                556 RVGMKLKEKKMAFWMSLY--OSORPEK 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879
FILING DATE: 17-MAY-1996
ATTOMAY AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REPERENCE/DOCKET NUMBER: 70432
TELEPHONE: 423-229-6189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,295A
FILING DATE: 25-April-97
CLASSIFICATION: 435
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COUNTRY:
USA
ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
"MPUTER: IBM Compatible
""A MINGOWS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08845295A
Patent No. 5817490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   584 amino acids
Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-08-845-295A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 EDCLYLMVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREK--VVLVFLQHR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGIFGFLSTDDSHARGNWGLLDQWAALRWVQENIAAFGGDPGNVTLFGQS--AGAMSISG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 KSEDELLDLTLKWKFLTLDFHGDQRESHPFLPTVVDGVLLPKMPEELLAEKDFTFNTVPY 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGVNNLEFNWLLPYIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLV--VEEYLD 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427 NVNEHDWKMLRNRWMDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHH----ARGIIVKP 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484 RIDGADHGDEMYFLFGGPFATGLSMGKEKALSLOMMKYWANFARTGNPNDGNLPCWP--R 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| ||||||: :|| | | : :| :|| | STATUMKFWANFARSGNPNGEGLFHWPFTM 536
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                                                                                                                                                                                                                                                                                                                                                                                                        ე
                                                                                                                                                                                                                                                                                                                                                                                                   2 WLL--PLVLTSLASSATWAGQPASPPVVDTAQGRVLGKYVSLEGLAFTQPVAVFLGVPFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 KPPLGSLRFAPPQPAEPWSFVKNTTSYPPMCCQDPVVEQMISDLFINFTGKERLT-LEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSGTKVMRVSNKMRFLQLNFQRDPBEIIWSMSPVVDGVVIPDDPLVLLTQG--KVSSVPY
                                                                                                                                                                                                                                                                                                                                                                        26 WILCWSLTLCLMAQTALGALHTKRPQVV-TKYGTLQGKQMHVG----KTPIQVFLGVPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                      81 RPPLGILRFAPPEPPEPWKGIRDATTYPPGCLQESWGQLASMYVST----RERYKWLRFS
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                                                            Length 584;
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                                                                                                                                                                                                                                                                                                               DB 3;
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11 Similarity 43.0%; Pred. No. 6.9e-111;
249; Conservative 108; Mismatches 193;
                                           08/845,295
           PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PILING DATE: 17-May-96; 25-April-97
ATTORNEY, AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECHNUNICATION INFORMATION:
03-Septmeber-98
                                                                                                                                                                   TELEPAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                            ; TOPOLOGY: Linear; MOLECULE TYPE: protein US-09-146-661-2
                                                                                                                                                                                                                                                                                                               Query Match
Best Local S:
Matches 249
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Sequence 2. Application US/09146661

Patent No. 6136575

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Bacorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of 2-Keto-L-Gu TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of 2-Keto-L-Gu NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bastman Chemical Company
STREET: P.O. Box 511
                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118
                                                                                                                                                                                                                                                                          252
                                                                                                                                                                                                                                                                                                                                     LSGTKVMRVSNKMRFLQLNFQRDPEIIWSMSPVVDGVVIPDDPLVLLTQG--KVSSVPY 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLGVNNLEFNWLLPYIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLV--VEEYLD 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            483
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                                                                                                                                                                                                              EDCLYLNVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREK--VVLVFLQHR
                                                                                                                                                                                                                                                                                                                  LGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQS--AGAMSISG
                                                                                                                                                                                                                                                                                                                                                                               LMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVAHLAGCNHNSTQI--LVNCLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 NVNEHDWKMLRNRMMDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHH---ARGIIVKP
                                                                                                                           26 WILCWSLTLCLMAQTALGALHTKRPQVV-TXYGTLQGKQMHVG----KTPIQVFLGVPFS
                                                                                                                                                                                         RPPLGILRFAPPEPPEPWKGIRDATTYPPGCLQESWGQLASMYVST----RERYKWLRFS
                                                                                               Gaps
                                                                                             29;
                                                                 DB 3; Length 584;
                                                                                             Indels
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APPLICATION NUMBER: US/09/146,661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microsoft Word
        ; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-09-140-933-2
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SOFTWARE: Microso
      Linear
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CITY: Ki
     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 MYVSTRERYKWLRFSEDCLYLNVYAPARAFGDPQLPVMVWFPGGAFIVGAASSYEGSDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AREKVVLVFLOHRLGI FGFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLF
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                                                                                                                                                                                 Sequence 2, Application US/10023515;
Patent No. 6644091
GENERAL INFORMATION;
APPLICANT: CURLIS, Rory A. J.
APPLICANT: CURLIS, Rory A. J.
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE;
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF;
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF;
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF;
CURRENT PELICATION NUMBER: 06/256,369
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOFIUM OBJET: 2001-03-28
NUMBER OF SEQ ID NOS: 6
LENGTH: 581
LENGTH: 581
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                                                           542 YNKDEKYLQLDFTTRVGMKLKEKKMAFWMSLYQSQRPEK 580
                                                                                Query Match
36.8%; Score 1145; DB 4;
Best Local Similarity 42.8%; Pred. No. 2.2e-108;
Matches 249; Conservative 91; Mismatches 186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-515-2
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US-10-023-515-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 KPPLGSLRFAPPQPAEPWSFVKNTTSYPPMCCQDPVVEQMISDLFTNFTGKERLT-LEFS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDCLYLNVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREK--VVLVFLQHR 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVAHLAGCNHNSTQI--LVNCLRA 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 KSEDELLDLTLKWKFLTLDFHGDQRESHPFLPTVVDGVILPKMPEEIIAEKDFTFNTVPY 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 WILCWSLTLCLMAQTALGALHTKRPQVV-TKYGTLQGKQMHVG----KTPIQVFLGVPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 WLL---PLVLTSLASSATWAGQPASPPVVDTAQGRVLGKYVSLEGLAFTQPVAVFLGVPPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 NVNEHDWKMLRNRMMDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHH---ARGIIVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.6%; Score 1169.5; DB 3; Length Best Local Similarity 43.0%; Pred. No. 6.9e-111; Matches 249; Conservative 108; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                                                                 08/845,295
   2-Keto-L-Gulonic Acid
                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRICR APPLICATION DATA:
PRICR APPLICATION DATA:
PRICR APPLICATION DATA:
PTLING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                   CITY: Kingsport
STATE: Tennesse
COUNTY: USA
ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: MINCROSEC WARD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/150,515
FILING DATE: 09-SEP-1998
                                                 E: Eastman Chemical Company
P.O. Box 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 584 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423-229-1239
TITLE OF INVENTION: 2-:
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-09-150-515-2
                                                     ADDRESSEE:
STREET: P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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Sequence 26, Application US/08446100 Patent No. 6001625
                                      Patent No. 6001625
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 WSHVKNTTSYPPMCSSDAVSGHMLSELFTNRKENIP-LKFSEDCLYLNIYTPADLTKRGF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 DOMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALF 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 RLFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQRDPE 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 SSLFRKNTKSLAEKIAIEAGCKTTTSAVMVHCLRQKTEEELMEVTLKMKFWALDLVGDPK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::| |::| | ::| | ::| | | | : | | | : | | :: | | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405 NVARHHRDAGAPTYMYEYRYRPSFSSDMRPKTVIGDHGDEIFSVLGAPFLKEGATEEEIK 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 LPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLP-YIMKFPLNRQAM 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 RKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDATFVYATL 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 HTKRPQVVTKYGTLQGKQMHVGK-----TPIQVFLGVPFSRPPLGILRFAPPEPPEP
                                                                                                                                                                                             US-09-264-737-1
; Sequence 1, Application US/09264737A
; Sequence 1, Application US/09264737A
; Sequence 1, Application US/09264737A
; General No. 6107549
; General Information:
    APPLICANT: Ruff. Theory Fraul C.C.
; APPLICANT: Ruff. Theory Information of Seterase Enzymes
    TITLE OF INVENTION: Expression of Seterase Enzymes
; TITLE OF INVENTION: Expression of Seterase Enzymes
; TITLE OF INVENTION: Expression of Seterase Enzymes
; TITLE OF INVENTION: Bayles: US/09/264,737A
; TITLE OF INVENTION: NUMBER: US/09/264,737A
; EARLIER APPLICATION NUMBER: 60/077,377
; EARLIER FILING DATE: 1998-03-10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
36.4%; Score 1133; DB 3; Length 539;
Best Local Similarity 41.3%; Pred. No. 3.3e-107;
Matches 227; Conservative 115; Mismatches 177; Indels 3
    506 NPNGNDLSLWPAYNLTEQYLQLDLMMSLGQRLKEPRVDFWTS 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --OSORPEK 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Rabbit
US-09-264-737-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287
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RESULT 8 US-08-446-100-26

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 VMRVSNKMRFLQLNFQRDPEBIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 EFNWLLP-YIMKFPLINRQAMRKETITKMLWSTRTLLNITKEOVPLVVEEYLDNVNEHDWK 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 EFGWLIPWQLMSYPLSEGQLDQXTAMSLLGSPIPLFAIAKELIPEATEKYLGGTD--DTV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 MLRNRNMDIVQDATFVYATLQTAHYHRDAGLPVYLYBFEHH-ARGIIVKPRTDGADHGDE 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 EDCLYLNVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 IFGFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 454;
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TILLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.6%; Score 983.5; DB 3;
43.6%; Pred. No. 5.6e-92;
ative 91; Mismatches 158;
                                                                                                                 ADDRESSED: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          broomfield
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
RAGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broo
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
TELEPHONE: (703) 425-4260
TELEPK: (703) 425-2767
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE: CHARACTER.STICS:
LENGTH: 454 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: human esterases
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Best Local Similarity 43.65
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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                                                                                                                                                                          CITY: Fairfax
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YES
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181 LLETTLKIGNSYLWTYRETQRHSTLIGTVIDGMLLLKTPEELQRERNFHTVPYMVGINKQ 240
                                                                                                                                                                                        359 LFSVFGAPFLKEGASEEEIRLSKOVMKFWANFARNGNPNGKGLPHWPEYNQKEGYLQIGA 418
                                                                      376 EFNWLLP-YIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWK 434
                                                                                                   241 EFGWLIPMQLMSYPLSEGQLDQKTAMSLLGSPIPLFAIAKELIPEATEKYLGGTD--DTV
                                                                                                                                                            435 MLRNRAMDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHH-ARGIIVKPRTDGADHGDE
                                                                                                                                                                                                                                                   494 MYFLFGGPPATGLSMGKEKALSLQMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLQLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                  CENTERL NO. "AUDITICATION US/08446100

GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Milard, Charles B
APPLICANT: Milard, Charles B
APPLICANT: Lockridge, Oksana
ITITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
CORRESPONDENCE: 31
CORRESPONDENCE: ADDRESS:
ADDRESSEE: 9669 A Main Street, P.O. Box 2509
CITY: Pairfax
STATE: VA
COUNTRY: US
ZIP: 22031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 454;
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPATER: TOP C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
31.6%; Score 983.5; DB 3;
Best Local Similarity 43.6%; Pred. No. 5.6e-92;
Matches 196; Conservative 91; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                  554 TTRVGMKLKEKKMAFWMSLYQSQRPEKQRQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broomfield
TELECOMONICATION INFORMATION:
TELEPHONE: (703) 425-4250
TELEPHONE: (703) 425-4267
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: human esterases
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HYPOTHETICAL: XE
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ORIGINAL SOURCE:
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                            494 MYFLFGGPFATGLSMGKEKALSLOMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLOLDF 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 VMRVSNKMRFLQLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNL 375
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                                                                                                                                                                                                                                     Sequence 30, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTE RE-BASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: US/08/MATION:
MANE: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
ATORNEY/DOCKET NUMBER: Broomfield
REGISTRATION NUMBER: 32,535
FILEFAX: (703) 425-4250
FILEFAX: (703) 425-4267
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91; Mismatches 158;
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Pred. No. 5.6e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
                                                                                                               554 TTRVGMKLKEKKMAFWMSLYQSQRPEKQRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human esterases
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Best Local Similarity 43.6%;
Matches 196; Conservative 9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YES
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COUNTRY: U
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US-08-446-100-30
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US-08-446-100-30
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137 EDCLYLNVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLG 196 Gaps

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                                                                                          PLASGLFHRAISQSGTALFRLFITSNPLK-VAKKVAHLAGCNHNSTQILVNCLRALSGTK 315
                                                                                                                                                 316 VMRVSNKMRFLQLNPQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNL 375
                                                                                                                                                                                                              BENWLLP-YIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWK 434
                                                                                                                                                                                                                                                                        435 MIRNRAMDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHH-ARGIIVKPRTDGADHGDE 493
                                                                                                                                                                                                                                                                                                                                    MYFLFGGPFATGLSMGKEKALSLOMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLOLDF 553
EHCLYLNIYTPADLTKKNRLPVMVMIHGGGLMVGAASTYDGLALAAHENVVVTIQYRLG 60
                                                                                                                                                                                                                                                                                             Sequence 27, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Milard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONDUTER READABLE FORM:

MEDIUN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
ATTONEY/AGENT INPOMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/POCKET NUMBER: 32,535
REFERENCE/POCKET NUMBER: 32,535
REFERENCE/POCKET NUMBER: 32,535
REFERENCE/POCKET NUMBER: 32,535
RELEPANCE (703) 425-2567
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
TEMBERM: 454 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Pairfax
STATE: VA
CUNTRY: US
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amino acid
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TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MLRNRAMDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHH-ARGIIVKPRTDGADHGDE 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYFLFGGPFATGLSMGKEKALSLQMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLQLDF 553
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                                                                                           Length 454;
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Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                  Indels
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                                                                                         31.5%; Score 981.5; DB 3;
43.6%; Pred. No. 8.9e-92;
live 91; Mismatches 158;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: broomfield FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Hendricks and Assoc.
9669 A Main Street, P.O.
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32-535
REFERENCE/DOCKET NUMBER: broom
                                    human esterases
N-terminal
                                                                                                                                      Conservative
                                                                                                                 Similarity
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                 ORIGINAL SOURCE:
ORGANISM: hum
FRAGMENT TYPE:
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US-08-446-100-28
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US-08-446-100-27
                                                                                                                   Best Local Sim.
Matches 196;
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PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                     single
        OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: N
ORIGINAL SOURCE:
ORGANISM: huma
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US-10-023-515-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 VMRVSNKMRFLQLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNL 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435 MLRNRMMDIVQDATFVYATLQTAHYHRDAGLPVYLYBFBHH-ARGIIVKPRTDGADHGDE 493
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Patent No. 6001625
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Broomfield, Charles B
APPLICANT: Lockridge, Okeana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
                                                                                                                                                                                                                                                  ; Score 977.5; DB 3; Length
; Pred. No. 2.3e-91;
90; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                554 TTRVGMKLKEKKMAFWMSLYQSQRPEKQRQ 583
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 43.6%;
Matches 196; Conservative 9
                                                                                                                                                                                                    ORGANISM: human esterases
                                                                                                                                                                       N-terminal
                                                                                                                        MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
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MEDIUM TYPE: Floppy COMPUTER: IBM PC com
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US-08-446-100-29
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ZIP: 220
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137 EDCLYLNVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLG 196
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Batent No. 6664021
GENERAL INFORMATION:
APPLICANT: CURTIS, ROLY A. J.
APPLICANT: Silos-Santiago, Inmaculada
ITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
SOFTWARE: Patentin Release #1.0, Version #1.25
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-YMAY-1995
CLASSIFICATION: 435
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43.6%; Pred. No. 2.3e-91;
tive 90; Mismatches 159;
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                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broomfield
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 425-4250
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
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Matches 196; Conservative 9
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completed: August
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US-09-491-356C-21
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Best Local S:
Matches 215,
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Patent No. 656661
GENERAL INFORMATION:
APPLICANT: Philibert, Robert A.
APPLICANT: Ginns, Edward I.
APPLICANT: Delist, Lynn
TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
FILE REPERENCE: 9465.61511
CURRENT APPLICATION NUMBER: US/09/491,356C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 VSTR-----ERYKWLRFSEDCLYLNVYAPARAPGDPQLPVNVWFPGGAFIVGAASS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGGDPGNVTLFGQSAGAMSISGLMMS-----PLASGLFHRAISQSGTAL--FRLFITSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 ARGRAKELARLIGCNETSSSELLDCIRSKSAEELLEATRSF----LEFEYVPFLPIFLAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 29.2%; Score 908.5; DB 4 Best Local Similarity 39.6%; Pred. No. 4.1e-84; Matches 226; Conservative 87; Mismatches 181
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FILE REFERENCE: 10448-122001
CURRENT APPLICATION WUMBER: US/10/023,515
CURRENT FILING DATE: 2001-12-18
FRIOR FILING DATE: 2000-12-18
FRIOR FILING DATE: 2000-12-18
FRIOR FILING DATE: 2001-03-28
FRIOR FILING DATE: 2001-03-8
FRIOR FILING DATE:
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US-09-491-356C-21
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                                                                                                                                                                                                                                                                                                                                                                  ---TALGALHTKR-POVVTKYGTLOGKOMHVGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---APGDPQL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---PVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNW
                                                                                                                                                                                                                                                                                                                                                                                                                         70 ---PIQVFLGVPFSRPPLGILRFAPPBPPBPWKGIRDATTYPPGCLQESWGQL---
                                                                                                                                                                                                                                                                                                      Indels 150;
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                                                                                                                                                                                                                                                              Score 849; DB 4; L. pred. No. 1e-77; 2; Mismatches 191;
CURRENT FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: PCT/US99/09365
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
LENGTH: 836
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al Similarity 33.2%; Pro
215; Conservative 92;
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ORGANISM: Rattus norvegicus
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Sequence 2, Appli
Sequence 254, Appl
Sequence 254, App
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1 MPSTVLPSTVLPSLLPTAGA......KMAFWMSLXQSQRPEKQRQF 584
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| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUBL_pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUBL_pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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16 US-10-343-593-10

9 US-09-978-593-254

9 US-09-978-697-254

9 US-09-998-328-254

10 US-09-998-328-254

10 US-09-998-328-254

10 US-09-978-1014-254

10 US-09-978-1014-254
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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US-10-001-227-2
Sequence 2, Application US/10001227
Sequence 2, Application Wo. US20030166900A1
GENERAL INFORMATION:
FPELICANT: RAPELLER-LIBERMANN
TAPLICANT: APPLICANTION:
TITLE OF INVENTION: METHODS OF USING 18903 TO TREAT PAIN AND
TITLE OF INVENTION: PAIN-RELATED DISORDERS
FILE REFERENCE: MNI-199
CURRENT APPLICATION NUMBER: US/10/001,227
CURRENT FILING DATE: 2001-11-30
FRIOR APPLICATION NUMBER: 60/250929
FRIOR APPLICATION NUMBER: 60/250929
FRIOR APPLICATION NUMBER: 60/250929
FRIOR APPLICATION NUMBER: 60/250929
FRIOR FILING DATE: 2000-11-30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 584
TYPE: PRT
CREANTEM: Homo sapiens
US-10-001-227-2
                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 3112; DB 14; Length 584; 100.0%; Pred. No. 2.5e-289; ive 0; Mismatches 0; Indels 0;
ALIGNMENTS
  Best Local Similarity 100.
Matches 584; Conservative
 Query Match
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120

61 GKOMHVGKTPIQVFLGVPFSRPPLGILRFAPPEPPEPWKGIRDATTYPPGCLQESWGQLA

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AAREKVVLVFLOHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTL 240
                            FGQSAGAMSISGLMASPLASGLFHRAISQSGTALFRIFIISNPLKVAKKVAHLAGCNHNS 300
                                                                                                                           241 FGQSAGAMSISGLWMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVAHLAGCNHNS 300
                                                                                                                                                                                      TQILVNCLRALSGTKVMRVSNKWRFLQLNFQRDPEBIIWSMSPVVDGVVIPDDPLVLLTQ 360
                                                                                                                                                                                                                     GKVSSVPYLLGVNNLEFNWLLPYIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLV 420
                                                                                                                                                                                                                                                                                                                     361 GKVSSVPXLLGVNNLEFNWLLPYIMKFPLNRQAMRKETITKALMSTRTLLNITKEQVPLV 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R.;
APPLICANT: BRUS, Christopher M.; DAS, Debopriya;
APPLICANT: BLEESANE, Angelo M.; DING, Li;
APPLICANT: ELLIOT, Vicki S.; GANDHI, Amena R.;
APPLICANT: ELLIOT, Vicki S.; GANDHI, Amena R.;
APPLICANT: ELLIOT, Vicki S.; GANDHI, Amena R.;
APPLICANT: LEE, Sally; LU, Dyung Aina M.;
APPLICANT: LEE, Sally; LU, Dyung Aina M.;
APPLICANT: LEE, Sally; LU, Dyung Aina M.;
APPLICANT: RAMKUMAL, Madhusudan M.; TANG, Huijun Z.;
APPLICANT: TRANGUALY, Madhusudan M.; TANG, Y. Tom,
APPLICANT: TRANGUALY, Garberine M.; TANG, Y. Tom,
APPLICANT: TRANGAVELU, Kavitha, TRORING, Machael,
APPLICANT: TREBOLEY, Carberine M.; CHAWIA, Narinder K.;
APPLICANT: TREBOLEY, Carberine M.; CHAWIA, Narinder K.;
APPLICANT: TREBOLEY, Carberine M.; CHAWIA,
APPLICANT: YAO, Monique G.; YUE, Henry
TITLE OF INVENTION BUGG G.; YUE, Henry
TITLE OF INVENTION UNMERR: US 60/223,055
PRIOR APPLICATION NUMBER: US 60/224,728
PRIOR PELING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US 60/224,728
PRIOR PELING DATE: 2000-08-13
PRIOR PELING DATE: 2000-08-14
PRIOR PELING DATE: 2000-08-31
PRIOR PELING DATE: 2000-08-31
PRIOR PELING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-15
PRIOR
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Publication No. US20040110259A1
GENERAL INFORMATION:
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TYPE: PRT ORGANISM: Homo sapiens FEATURE:

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GKQMHVGKTPIQVFLGVPFSRPPLGILRFAPPEPPEPWKGIRDATTYPPGCLQESWGQLA 120
                                                                                                                                                                                                                                                                                  SMYVSTRERYKWLRFSEDCLYLNVYARARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDL 180
                                                                                                                                                                                                                                  61 GKQMHVGKTPIQVFLGVPFGYPFSRPPLGILRFAPPEPPFPWKGIRDATTYPPGCLQESWGQLA 120
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                                                                                                                 Gaps
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                                                                            Length 584;
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                                                                      100.0%; Score 3112; DB 16;
100.0%; Pred. No. 2.5e-289;
ive 0; Mismatches 0;
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7478588CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fong, Sherman
Gao, Wel-Qiang
Gerber, Hanspeter
Gerritsen, Mary B.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 254, Application US/09978295A Patent No. US20020156006A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferrara, Napoleon
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Botstein, David
Desnoyers, Luc
Eaton, Dan
                                                                    Query Match
Best Local Similarity 100.
Matches 584; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bottetein, David
APPLICANT: Bottetein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleo
APPLICANT: Ferrara, Napoleo
APPLICANT: Filvaroff, Ellen
APPLICANT: Folgs, Sherman
APPLICANT: Gao, Wei-Ciang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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US-09-978-295A-254
                                     US-10-343-593-10
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 60/08033
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081049
PRIOR APPLICATION NUMBER: 60/081049
PRIOR APPLICATION NUMBER: 60/081049
PRIOR APPLICATION NUMBER: 60/081049
PRIOR PLING DATE: 1998-04-06
PRIOR APPLICATION NUMBER: 60/081051
PRIOR APPLICATION NUMBER: 60/081051
PRIOR FILING DATE: 1998-04-06
PRIOR FILING DATE: 1998-04-06
PRIOR FILING DATE: 1998-04-06
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-05
PRIOR PLING DATE: 1998-04-05
PRIOR PLING DATE: 1998-04-05
PRIOR PLING DATE: 1998-04-05
PRIOR PLING DATE: 1998-04-15
PRIOR PLING DATE: 1998-04-27
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1
                                                                                                                Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 254, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams, P. Mickey Wood, William I.
                                                                                                                                                                                                                                                                                                             Ferrara, Napoleon
Filvaroff, Ellen
                                                                                                                                                                   APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daniel
                                                                                                                                                                                                                                                                                     Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumas,
                                                             US-09-978-697-254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 VGKTPIQVFLGVPFSRPPLGILRFAPPEPPEPWKGIRDATTYPPG------- 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 RLTATSASRVQASLLPQPLSVWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVY 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 APARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 SHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 AISQSGTALFRLFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMFF 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 65.1%; Score 2026.5; DB 9; Length 545; Best Local Similarity 80.3%; Pred. No. 3.6e-185; Matches 399; Conservative 5; Mismatches 26; Indels 67;
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-13
PRIOR PLING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08550
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PLING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR APPLICATION NUMBER: 60/08557
PRIOR APPLICATION NUMBER: 60/08557
PRIOR PLING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08557
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APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same PLICATION NUMBER: US/09/978,697

CURRENT FILING DATE: 2001-10-16

PRIOR PELLING DATE: 2001-10-17

PRIOR PLILNG DATE: 1997-10-17

PRIOR PLILNG DATE: 1997-10-17

PRIOR PLILNG DATE: 1997-10-17

PRIOR PLILNG DATE: 1997-10-17

PRIOR PRILNG DATE: 1997-10-17

PRIOR PLILNG DATE: 1998-03-10

PRIOR PLILNG DATE: 1998-03-11

PRIOR PLILNG DATE: 1998-03-11

PRIOR PLILNG DATE: 1998-03-11

PRIOR PLILNG DATE: 1998-03-17

PRIOR PLILNG DATE: 1998-03-27

PRIOR PLILNG DATE: 1998-03-20

PRIOR PLING DATE: 1998-03-20

PRIOR PLILNG DATE: 1998-03-20

PRIOR PLING DATE: 1998-03-20

PRIOR PLING DATE: 1998-03-20
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hangspeer
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kijavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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R APPLICATION NUMBER: 60/082797
R FILING DATE: 1998-04-22
R FILING DATE: 1998-04-22
R FILING DATE: 1998-04-23
R RFLING DATE: 1998-04-23
R APPLICATION NUMBER: 60/08336
R FILING DATE: 1998-04-27
R R FILING DATE: 1998-04-28
R APPLICATION NUMBER: 60/083322
R R FILING DATE: 1998-04-28
R APPLICATION NUMBER: 60/083322
R R RILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083328
R RILING DATE: 1998-04-29
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REPLICATION NUMBER: 60/081195

REPLICATION NUMBER: 60/081203

REPLICATION NUMBER: 60/081203

REPLICATION NUMBER: 60/081229

REPLICATION NUMBER: 60/081229

REPLICATION NUMBER: 60/081229

REPLICATION NUMBER: 60/081817

REPLICATION NUMBER: 60/081817

REPLICATION NUMBER: 60/081819

REPLICATION NUMBER: 60/08268

REPLICATION NUMBER: 60/08268

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REPLICATION NUMBER: 60/082804

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                                                                                                                                                                                                                                                                                                                                                                                                       R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080107
RR FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080165
R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080194
R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LING DATE: 1998-04-01
PPLICATION NUMBER: 60/081070
LING DATE: 1998-04-08
                                                                                                            FILING DATE: 1998-03-27
APPLICATION WINBER: 60/079728
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079786
                                                                                                                                                                                                                                  FILING DATE: 1998-03-27
APPLICATION UNMBER: 60/079920
APPLING DATE: 1998-03-30
APPLICATION NUMBER: 60/079923
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PPLICATION NUMBER: 60/080328
LING DATE: 1998-04-01
PPLICATION NUMBER: 60/080333
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PLICATION NUMBER: 60/080334
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LING DATE: 1998-04-08
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079689
                                                                                APPLICATION NUMBER: 60/079663
FILING DATE: 1998-03-27
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/080105
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PELICATION NUMBER: 60/081071
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                                                           LING DATE: 1998-03-27
                                                       PRIOR
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47 LGSTSTPATTSAPSSGFGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLQGKQMH ------CLOESWGOLASMYVSTRERYKWLRFSEDCLYLNVY LPSTVLPSLLPTAGAGWSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMH 67; Length 545 66 VGKTPIQVFLGVPFSRPPLGILRFAPPEPPEPWKGIRDATTYPPG---Indels DB 9; 56; Score 2026.5; DB 9 Pred. No. 3.6e-185; 5; Mismatches 26; PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR APPLICATION NUMBER: 60/08350
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-05-06
PRIOR PRIOR DATE: 1998-05-06
PRIOR PLING DATE: 1998-05-06
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-13
PRIOR PLING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15 Query Match
Best Local Similarity 80.3%;
Matches 399; Conservative v 111 g 엄 ò 8 ò

Gaps

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PRIOR
                                                                    265
                   AISQSGTALFRIFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRF 325
                                                                                                                                                       LQLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVMNLEFNWLLPYIM 385
                                                                                                                                                                                                                        407 LQLNFQRDPEBIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPY-- 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPRENCE: PS560PLC9

FILE REPRENCE: PS560PLC9

CURRENT APPLICATION NUMBER: U5/09/978,192A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-110-17

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-13
APARAPGDPQLPV//WFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD
                                                                                    386 KFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQ
                                                                SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kljavin, Ivar J.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 254, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   446 DATFVYATLQTAHYHRD 462
                                                                                                                                                                                                                                                                                                                                                           500 DATFVYATLQTAHYHRE 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams, P. Mickey Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Filvaroff, Ellen
Fong, Sherman
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APPLICANT: Baker Kevin P.
APPLICANT: Betsein, David
APPLICANT: Beton, Dan
APPLICANT: Baton, Dan
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US-09-978-192A-254
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R FILING DATE: 1998-03-10
R APPLICATION NUMBER: 60/077632
R APPLICATION NUMBER: 60/077641
R APPLICATION NUMBER: 60/077641
R FILING DATE: 1998-03-11
R FILING DATE: 1998-03-11
R FILING DATE: 1998-03-11
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R FILING DATE: 1998-03-13

R APPLICATION NUMBER: 60/07886

R FILING DATE: 1998-03-20

R RILING DATE: 1998-03-20

R RELING DATE: 1998-03-20

R APPLICATION NUMBER: 60/078939

R FILING DATE: 1998-03-20

R APPLICATION NUMBER: 60/07994

R FILING DATE: 1998-03-25

R APPLICATION NUMBER: 60/079656
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A APPLICATION NUMBER: 60/079923
R FILING DATE: 1998-03-30
A APPLICATION NUMBER: 60/080105
R FILING DATE: 1998-03-31
A APPLICATION NUMBER: 60/080107
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APPLICATION NUMBER: 60/079689
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079663
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APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079920
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APPLICATION NUMBER: 60/080165
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APPLICATION NUMBER: 60/080328
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APPLICATION NUMBER: 60/081070
FILING DATE: 1998-04-08
FILING DATE: 1998-04-08
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FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/081203
FILING DATE: 1998-04-09
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/080327
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APPLICATION NUMBER: 60/080334
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APPLICATION NUMBER: 60/081817
FILING DATE: 1998-04-15
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
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PRING APPLICATION NUMBER: 60/081838
PRIOR APPLICATION NUMBER: 60/08268
PRIOR FILING DATE: 1998-04-21
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PRIOR PELLING DATE: 1998-04-22
PRIOR PELLING DATE: 1998-04-22
PRIOR PELLING DATE: 1998-04-22
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PRIOR PELLORITON NUMBER: 60/082797
PRIOR PILLING DATE: 1998-04-23
PRIOR PILLING DATE: 1998-04-23
PRIOR PILLING DATE: 1998-04-29
PRIOR PELLORITON NUMBER: 60/08336
PRIOR PILLING DATE: 1998-04-29
PRIOR PELLORITON NUMBER: 60/08345
PRIOR PILLING DATE: 1998-04-29
PRIOR PELLORITON NUMBER: 60/08345
PRIOR PELLING DATE: 1998-04-29
PRIOR PELLING DATE: 1998-05-07
PRIOR PELLOR DATE: 1998-05-07
PRIOR PELLING D
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VGKTPIOVFLGVPFSRPPLGILRFAPPEPPEPWKGIRDATTYPPG------- 110 286 SHARGNWGLLDOMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 265 AISOSGTALFRLFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRF 325 326 LOLNFORDPERIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEPNWLLPYIM 385 407 LOLNFORDPEELIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPY-- 464 386 KFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQ 445 465 ------NITKEQVPLVVEEYLDNVNEHDWKMLRNRMYDIVQ 499 226 APARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD 205 6 DPSTVLPSLLPTAGAGWSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMH Gaps ,67; Length 545; 26; Indels DB 9; Query Match
Best Local Similarity 80.3%; Pred. No. 3.6e-185; Matches 399; Conservative 5; Mismatches 26; Ferrara, Napoleon Filvaroff, Ellen Fong, Sherman Gao, Wai-Qiang Gerber, Hanspeter Gerritsen, Mary E. Goddowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L. Hillan, Kenneth J RESULT 6
US-09-832A-254
; Sequence 254, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION: PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR APPLICATION NUMBER: 60/085697 500 DATFVYATLQTAHYHRE 516 446 DATFVYATLOTAHYHRD 462 APPLICANT: Baker Kevin P.
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Beton, Dan
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Forg, Sherman
APPLICANT: Filvaroff, Blien
APPLICANT: Foog, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen; Mary E.
APPLICANT: Gerritsen; Mary E.
APPLICANT: Gerritsen; Mary E.
APPLICANT: Germaldi, J. Chris
APPLICANT: Gimaldi, J. Chris
APPLICANT: Grimaldi, J. Chris
APPLICANT: Grimaldi, J. Chris
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J. 99 266 47 146 206 원 ò d ò g δ g ò g à g ò g ò d à

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APPLICATION NUMBER: 60/080328
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Ruoi Sophia S.

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R FILING DATE: 1998-04-27

R APPLICATION NUMBER: 60/083322

R FILING DATE: 1998-04-28

R APPLICATION NUMBER: 60/083392

R FILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/083495

R APPLICATION NUMBER: 60/083496

R APPLICATION NUMBER: 60/083499

R PILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/083499

R PELLING DATE: 1998-04-29 R APPLICATION NUMBER: 60/080334
R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/081070
R APPLICATION NUMBER: 60/081049
R APPLICATION NUMBER: 60/081049
R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081049 R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081203
R FILING DATE: 1998-04-09
R PILING DATE: 1998-04-09
R FILING DATE: 1998-04-09
R APPLICATION NUMBER: 60/081955 R APPLICATION NUMBER: 60/081819
R FILING DATE: 1998-04-15
R FILING DATE: 1998-04-15
R FILING DATE: 1998-04-15
R APPLICATION NUMBER: 60/081838
R FILING DATE: 1998-04-15 R FILING DATE: 1998-04-21
R APPLICATION NUMBER: 60/082704
R FILING DATE: 1998-04-22
R APPLICATION NUMBER: 60/082804
R FILING DATE: 1998-04-22
R APPLICATION NUMBER: 60/082700 DATE: 1998-04-01 ATION NUMBER: 60/080333 DATE: 1998-04-01 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081195 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/082797 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082796 APPLICATION NUMBER: 60/083558 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083559 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-23 APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083554 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083500 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083742 FILING DATE: 1998-04-30 1998-04-22 FILING DATE:

500 DATFVYATLQTAHYHRE 516

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PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR PELLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR APPLICATION NUMBER: 60/084640
PRIOR PELLING DATE: 1998-05-07
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PRIOR PILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-15
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-----NITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQ 499
                                                                                                                47 LGSTSTPATTSAPSSGFGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLQGKQMH 106
                                                                                                                                                                                                                                                                                                                          146 APARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD 205
                                                                                                                                                                                                                                                                                                                                                                                                        SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                            SHARGNWGLLDOMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 AISOSGTALFRIFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRF 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPYIM 385
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                                                                                                                                                                                        167 RLTATSASRVQASLLPQPLSVWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVY
                                                                                  6 LPSTVLPSLLPTAGAGWSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMH
                                                                                                                                                                                                                                               111 ------CLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVY
                                                                                                                                                               66 VGKTPIQVFLGVPFSRPPLGILRFAPPBPPBPWKGIRDATTYPPG------
65.1%; Score 2026.5; DB 9; Length 545; 80.3%; Pred. No. 3.6e-185; tive 5; Mismatches 26; Indels 67;
      Query Match
Best Local Similarity 80.3
Matches 399; Conservative
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kljavin, Ivar J.
Kuo, Sophia S.
US-09-978-189-254; Sequence 254, Application US/09978189; Publication No. US20030004102A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                      APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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PRIOR FILING DATE: 1996-03-26
PRIOR FILING DATE: 1996-03-27
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PRIOR PRILING DATE: 1996-03-27
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PRIOR FILING DATE: 1996-03-27
PRIOR PLING DATE: 1996-03-31
PRIOR PLING DATE: 1996-04-01
PRIOR PAPLICATION UNMERS: 60/08127
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6 LPSTVLPSLLPTAGAGWSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMH 67; Gaps DB 10; Length 545; Query Match
Best Local Similarity 80.3%; Pred. No. 3.6e-185;
Matches 399; Conservative 5; Mismatches 26; Indels R PILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083496
R APPLICATION NUMBER: 60/083499
R FILING DATE: 1998-04-29
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R APPLICATION NUMBER: 60/08354
R FILING DATE: 1998-04-29
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R FILING DATE: 1998-05-13
R APPLICATION NUMBER: 60/085323
R APPLICATION NUMBER: 60/085582
R APPLICATION NUMBER: 60/085582 THE FILING DATE: 1998-05-05

RAPELICATION NUMBER: 60/064414

RAPLICATION NUMBER: 60/064411

RAPLICATION NUMBER: 60/06441

RAPLICATION NUMBER: 60/084637

RELING DATE: 1998-05-06

RAPLICATION NUMBER: 60/084639

RAPLICATION NUMBER: 60/084639

RAPLICATION NUMBER: 60/084639

RAPLICATION NUMBER: 60/084640

RAPLICATION DATE: 1998-05-07 R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083500
R FILING DATE: 1998-04-29
R FILING DATE: 1998-04-29
R FILING DATE: 1998-04-30
R APPLICATION NUMBER: 60/084366 APPLICATION NUMBER: 60/084627 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084643 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/085339 FILING DATE: 1998-05-13 60/085579 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085697 APPLICATION NUMBER: 60/085704 1998-05-15 APPLICATION NUMBER: à

47 LGSTSTPATTSAPSSGFGTGLFGSKPATGFTLGGTNTGALHTKRPOVVTKYGTLGGKOMH 106

8 6 8

------CLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVY 145

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66 VGKTPIQVFLGVPFSRPPLGILRFAPPEPPEPWKGIRDATTYPPG---

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386 KPPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQ 445
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                                                                                                                                                                                                                                                                               266 AISOSGTALFRIFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRF 325
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                                                                                                                            66 VGKTPIQVFLGVPFSRPPLGILRPAPPEPPFPWKGIRDATTYPPG------- 110
                                                                                                                                                 146 APARAPGDPOLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLOHRLGIFGFLSTDD
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                                                              6 LPSTVLPSLLPTAGAGWSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMH
                                Gaps
                                67;
Length 545;
                                Indels
   DB 10;
Score 2026.5; DB 10;
Pred. No. 3.6e-185;
5; Mismatches 26;
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Filvaroff, Ellen
Filvaroff, Ellen
Gao, Wei-Qiang
Gerber, Hanspeter
Gezritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
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   Query Match
Best Local Similarity 80.3%;
Matches 399; Conservative 5
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Kuo, Sophia S.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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US-09-978-585A-254
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                                                       APARAPGDPQLPVMVWFPGGAPIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD 205
                                                                             206 SHARGNWGLLDQWAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMWSPLASGLFHR 265
                                                                                                                                                    287 SHARGIWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 346
                                                                                                                                                                                                                                                                        APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P263091C22
CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Mapoleon
APPLICANT: Filvarca, Mapoleon
APPLICANT: Filvarca, Sallen
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Filvaroff, Ellen
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Kuo, Sophia S.
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Gao, Wei-Qiang
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ORGANISM: Homo sapiens
US-09-978-608A-254
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US-09-978-608A-254
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 3.6e-185;
5; Mismatches 26; Indels
                           FILE REFERENCE: P263091C15
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624.
PRIOR APPLICATION removed - See File Wrapper or Palm
SEQ ID NO 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 254, Application US/09978191A
Publication No. US20030050239A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
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Best Local Similarity 80.3%;
Matches 399; Conservative
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Botstein, David
Desnoyers, Luc
Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerritsen, Manspeter
Gerritsen, Mary E.
Goddard, Audrey
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APPLICANT: Baker Kevin P
                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-254
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US-09-978-191A-254
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APPLICANT: MINITEY, MARSIN L.
APPLICANT: Milloria S.
APPLICANT: Major. Mary A.
APPLICANT: Major. Maj
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PRIOR PELICATION NUMBER: 60/080327
PRIOR PLING DATE: 1998-04-01
PRIOR PELICATION NUMBER: 60/080338
PRIOR APPLICATION NUMBER: 60/080338
PRIOR APPLICATION NUMBER: 60/080334
PRIOR APPLICATION NUMBER: 60/081049
PRIOR PLING DATE: 1998-04-01
PRIOR PLING DATE: 1998-04-01
PRIOR PLING DATE: 1998-04-08
PRIOR PLING DATE: 1998-04-09
PRIOR PLING DATE: 1998-04-09
PRIOR PLING DATE: 1998-04-15
PRIOR PLING DATE: 1998-04-22
PRIOR PLING DATE: 1998-04-29
PRIOR PLING
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146 APARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD 205 287 SHARGNWGLLDQMAALRWVQENIAAFGGDFGNVTLFGQSAGAMSISGLMMSPLASGLFHR 346 AISQSGTALFRLFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRF 325 KPPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQ 445 LOINFORDPEELIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPYIM 385 ------CLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVY SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 347 AISQSGTALFRLFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVNRVSNKMRF 6 LPSTVLPSLLPTAGAGWSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQWH 47 LGSTSTPATTSAPSSGFGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLQGKQMH Query Match 65.1%; Score 2026.5; DB 10; Length 545; Best Local Similarity 80.3%; Pred. No. 3.6e-185; Matches 399; Conservative 5; Mismatches 26; Indels 67; PRIOR PILING DATE: 1998-05-07 PRIOR PILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084639 PRIOR APPLICATION NUMBER: 60/084640 PRIOR PILING DATE: 1998-05-07 PRIOR PILING DATE: 1998-05-13 PRIOR PILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-AFFLING DATE: 1998-05-00 APPLICATION NUMBER: 60/084637 99 386 206 997 407 111 326 g 8 a g ò d à ò 8 g 슝 ò

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REPLING DATE: 1998-03-27
RAPLICATION NUMBER: 60/079663
RAPLICATION NUMBER: 60/079663
RAPLICATION NUMBER: 60/07968
RELING DATE: 1998-03-27
RAPLICATION NUMBER: 60/079920
RELING DATE: 1998-03-30
RAPLICATION NUMBER: 60/079920
RELING DATE: 1998-03-30
RAPLICATION NUMBER: 60/079923
RELING DATE: 1998-03-30
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RELING DATE: 1998-03-31
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R PILING DATE: 1998-04-01
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R FILING DATE: 1998-04-15
RR APPLICATION NUMBER: 60/081817
RR APPLICATION NUMBER: 60/081819
RR APPLICATION NUMBER: 60/081819
RR FILING DATE: 1998-04-15
RR FILING DATE: 1998-04-15
RR FILING DATE: 1998-04-15
RR FILING DATE: 1998-04-15
RR FILING DATE: 1998-04-21
RR APPLICATION NUMBER: 60/082568
RR FILING DATE: 1998-04-21
RR APPLICATION NUMBER: 60/08269
RR FILING DATE: 1998-04-21
RR APPLICATION NUMBER: 60/08269
RR FILING DATE: 1998-04-22
RR APPLICATION NUMBER: 60/082804
RR FILING DATE: 1998-04-22
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R APPLICATION NUMBER: 60/081071
R FILING DATE: 1998-04-08
R PILING DATE: 1998-04-08
R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081203
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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082796
FILING DATE: 1998-04-23
APPLICATION NUMBER: 60/083336
FILING DATE: 1998-04-27
                                                                                                   APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079689
                                 PLICATION NUMBER: 60/079656
LING DATE: 1998-03-26
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APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/081229
FILING DATE: 1998-04-09
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APPLICATION NUMBER: 60/081049
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PRIOR APPLICATION NUMBER: 60/083322
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US-09-978-443A-254
S. Sequence 254, Application US/09978403A
Publication No. US20030050240A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin J.
Hillan, Kenneth J
Kljavin, Ivar J.
Kljavin, Ivar J.
Kljavin, Amry A.
Papier, Mary A.
                                            500 DATFVYATLQTAHYHRE 516
446 DATFVYATLQTAHYHRD 462
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Desnoyers, Luc
Eaton, Dan
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, Davi
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287 SHARGNWGLLDQMAALRWVQENIAAFGGDFGNVTLFGQSAGAMSISGLMMSFLASGLFHR 346
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                                                                                                                                                                                                                                                                                                                                                 266 AISOSGTALFRIFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMF 325
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107 VGKTPIQVFLGVPFSRPPLGILRFAPPEPPEPWKGIRDATTYPPGWSLALSPGWSAVARS 166
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acide Encoding the Same
FILE REFERENCE: P2630PIC25
CURRENT APPLICATION NUMBER: U3/09/978,564A
CURRENT APPLICATION NUMBER: U3/09/978,564A
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-179
PRIOR FILING DATE: 1997-10-179
PRIOR PLING DATE: 1997-10-179
PRIOR PLING DATE: 09/062250
                                                                                       167 RITATSASRVQASLLPQPLSVWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVV
                                                                                                                                                 146 APARAPGDPQLPVMVWPPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD
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Publication No. US20030050241A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Bestein, David
APPLICANT: Berstein, David
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kljavin, Ivar J.
Kno, Sophia S.
Napier, Mary A.
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
Goddard, Audrey
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                                       PRIOR APPLICATION NUMBER: 60/083495
PRIOR APPLICATION NUMBER: 60/08345
PRIOR APPLICATION NUMBER: 60/083545
PRIOR PILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08441
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PPLICATION NUMBER: 60/08559
PRIOR PILING DATE: 1998-05-15
PRIOR PPLICATION NUMBER: 60/08559
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                             PLICATION NUMBER: 60/083392
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1997-11-03 NUMBER: 60/06531 1997-11-13 NUMBER: 60/06636. 1998-03-10 NUMBER: 60/07764. 1998-03-11 NUMBER: 60/07764. 1998-03-11 NUMBER: 60/07764. 1998-03-11 NUMBER: 60/07764. 1998-03-11 NUMBER: 60/0779	NUMBER: 60/07893 NUMBER: 60/07891 1998-03-20 NUMBER: 60/0793 1998-03-20 NUMBER: 60/07929 NUMBER: 60/07965 1998-03-26 NUMBER: 60/07966 1998-03-26 NUMBER: 60/07968 1998-03-27 NUMBER: 60/07968 1998-03-27 NUMBER: 60/07968 1998-03-27 NUMBER: 60/07968 1998-03-27 NUMBER: 60/07968 1998-03-27 NUMBER: 60/07968	NUMBER 1998 - NU
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PRIOR APPLICATION NUMBER: 60/081919
PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-04-15
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PRIOR PILING DATE: 1998-04-21
PRIOR PILING DATE: 1998-04-21
PRIOR FILING DATE: 1998-04-21
PRIOR PILING DATE: 1998-04-22
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-05-07

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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 APARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 APARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD
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80.3%; Pred. No. 3.6e-185;
tive 5; Mismatches 26;
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Publication No US20030054405A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Beter Kevin P.
APPLICANT: Beter the David
APPLICANT: Beterin, David
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Food, Wel-Qiang
APPLICANT: Gao, Wel-Qiang
APPLICANT: Gao, Wel-Qiang
APPLICANT: Gacher, Marspeter
APPLICANT: Gerber, Marspeter
APPLICANT: Gerber, Mary E.
APPLICANT: Gerber, Mary E.
                     PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR PAPPLICATION NUMBER: 60/08569
PRIOR PAPPLICATION NUMBER: 60/085579
PRIOR PAPLICATION NUMBER: 60/08559
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
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        FILING DATE: 1998-05-15
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Best Local Similarity 80.3
Matches 399; Conservative
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PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-07
PRIOR PLICATION NUMBER: 60/084637
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PRIOR PLICATION NUMBER: 60/084640
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PRIOR PLICATION NUMBER: 60/084600
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PRIOR PLILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/08559
PRIOR PLILING DATE: 1998-05-15
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226 205 286 265 326 LOLNFORDPETITWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPYIM 385 386 KPPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQ 445 66 VGKTPIQVFLGVPFSRPPLGILRFAPPEPPEPWKGIRDATTYPPG------107 VGKTPIQVFLGVPFSRPPLGILRFAPPEPPEPWKGIRDATTYPPGWSLALSPGWSAVARS 111 --------CLOESWGOLASMYVSTRERYKWLRFSEDCLYLNVY 146 APARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD 227 APARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD 206 SHARGNWGLLDOWAALRWVOENIAAFGGDPGNVTLFGOSAGAMSISGLMMSPLASGLFHR 6 LPSTVLPSLLPTAGAGWSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMH 266 AISOSGTALFRIFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRF 67; Gaps DB 10; Length 545; 26; Indels Query Match
Best Local Similarity 80.3%; Pred. No. 3.6e-185;
Matches 399; Conservative 5; Mismatches 26; Dp g ò 8

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PRIOR PILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR PILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081070
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PRIOR APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/079656
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APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/083336
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FILING DATE: 1998-03-25
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FILING DATE: 1998-03-27
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                                  1998-03-2
                                                                                                                                                                                                          1998-03-
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APPLICANT: Stewart, Timothy A.
APPLICANT: Timas, Daniel
APPLICANT: Timas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P263-0916122
CURRENT APPLICATION NUMBER: US/09/981,915A
CURRENT APPLICATION NUMBER: 2001-10-16
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PRIOR APPLICATION NUMBER: 09/91858
PRIOR PILING DATE: 2001-10-16
PRIOR PELING DATE: 2001-0-30
PRIOR PILING DATE: 2001-0-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-13
PRIOR PELING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/07753
PRIOR PELING DATE: 1998-03-11
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Gurney, Austin L.
Hillan, Kenneth J
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Pan, James,
Pan, James,
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
...art, Timothy A.
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Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wel-Qiang
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Goddard, Audrey
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                                  465 -----
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Napier, Mary A.
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LPSTVLPSLLPTAGAGWSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMH

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107 VGKTPIQVFLGVPFSRPPLGILRFAPPEPPEPWKGIRDATTYPPGWSLALSPGWSAVARS 166
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                                                                                                        167 RLTATSASRVQASLLPQPLSVWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVY
                                                                                                                                                   146 APARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDD
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CURRENT APPLICATION NUMBER: US/09/978,824
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 60/062250
                                                                                                                                                                                                                                                                                                        266 AISOSGIALFRIFIISNPLKVAKKVAHLAGCNHNSTOILVNCLRALSGIKVMRVSNKMRF
                                                                         -----CLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVY
66 VGKTPIQVFLGVPFSRPPLGILRFAPPEPPEPWKGIRDATTYPPG
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Kuo, Sophia S.
Napier, Mary A.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
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PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 APARAPGDPQLPVMVWPPGGAFIVGAASSYEGSDLAAREXVVLVFLQHRLGIFGFLSTDD 205
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65.1%; Score 2026.5; DB 10; Length 545;
Best Local Similarity 80.3%; Pred. No. 3.6e-185;
Matches 399; Conservative 5; Mismatches 26; Indels 67;
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Job time : 52 secs
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
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SUMMARIES

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30 6572 21.6 620 2 A54413 31 655.5 21.4 581 2 G39768 33 653.5 21.0 664 2 UC7990 34 651.5 20.9 506 2 H75522 35 620.5 19.9 540 2 S51043 36 620.5 19.9 540 2 S51043 37 604 19.4 637 2 S56236 38 601.5 19.0 691 2 B61050 41 580.5 18.7 578 2 F89068 42 579 18.6 602 2 H7555 43 579 18.6 602 2 H7555 44 578.5 18.6 540 2 H7556 45 568.5 18.3 502 2 AB0666	acetylcholinestera	cholinesterase (EC	para-nitrobenzyl e	acetylcholinestera	probable carboxyle	triacylglycerol li	carboxylesterase (acetylcholinestera	acetylcholinestera	acetylcholinestera	protein T28C12.4b	hypothetical prote	carboxylesterase,	acetylcholinestera	acetylcholinestera	probable esterase
11110000000000000000000000000000000000	A54413	C39768	B69680	JC7990	H75522	S25062	S51043	866236	S47639	JE0150	F89068	T32053	A75250	T37254	A25363	AE0666
11110000000000000000000000000000000000	7	0	~	~	7	Н	7	~	7	7	~	7	7	~1	7	7
	620	581	489	664	909	593	540	637	767	691	578	658	540	602	746	202
330 331 66 67 334 673 334 673 336 673 673 673 673 673 673	21.6	21.4	21.0	21.0	20.9	20.6	19.9	19.4	19.3	19.0	18.7	18.7	18.6	18.6	18.6	18.3
0 1 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	672	665.5	653.5	653	651.5	640	620.5	604	601.5	590	580.5	580.5	579	579	578.5	568.5
	30	31	35	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 A47162 thiolesterase B C;Species: Anas C;Dates: 05-May- C;Acces: 01-May- C;Acces: 01-May- R;Hwang, C.S.; R R;Hwang, C.S.; R A;Title: Molecul- A;Reference numl A;Residues: 1-5;A;Csuperfamily: C;Reywords: hyd	thiolesterase B (EC 3) precursor - mallard C;Species: Anas platyrhynchos (mallard) C;Species: Anas platyrhynchos (mallard) C;Species: Anas platyrhynchos (mallard) C;Accession: A47162 R;Hwang, C.S.; Kolattukudy, P.E. T;Hwang, C.S.; Kolattukudy, P.E. R;Hwang, C.S.; Kolattukudy, P.E. R;Hwang, C.S.; Kolattukudy, P.E. R;Hwang, C.S.; Kolattukudy, P.E. A;Title: Molecular cloning and sequencing of thiossterase B cDNA and stimulation of exp. A;Title: Molecular cloning and sequencing of thiossterase B cDNA and stimulation of exp. A;Reference number: A47162; MUID:93300823; PMID:8314791 A;Residues: 1-557 cHWA A;Residues: 1-557 cHWA A;Residues: 1-557 cHWA C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: hydrolase C;Keywords: hydrolase F;Se-545/Domain: cholinesterase homology <che></che>
Query 1 Best Lo Matche	Query Match 41.5%; Score 1290.5; DB 2; Length 557; Best Local Similarity 46.0%; Pred. No. 1.4e-96; Matches 260; Conservative 106; Mismatches 172; Indels 27; Gaps 11;
& 93	27 ILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGXQMHVGKTPIQVFLGVPFSRPPL 84 :
% q	85 GILRFADPEPPEPWKGIRDATTYPPGCLQES-WQQLASWYVSTRERYKWLRFSEDCLYLN 143
S SS	144 VYAPARAPGDFQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLST 203
oy du	204 DDSHARGNWGLIDQMAALRWVQENIAAFGGBFGNVTLFGQSAGAMSISGLMMSPLASGLF 263
op og	264 HRAISGSGTALFRIFILTSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKM 323
oy Qu	324 RFLQINFQRDPEEIIWSWSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPY 383 306PPMFISASLDGVFFRXSPRQLLSEKVINAVPYIIGVNNCEFGMILPR 352
S Q	364 IMKFPLNRQAMRKETITKALWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKALRNRMM 441 1
·δ	442 DIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHHARGIIVKPRTDGADHGDEMYFLF 498

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177

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A; Molecule type: mRNA
A; Residues: 1-567 < MUN>
A; Residues: 1-567 < MUN>
A; Cross-references: GB:M73499; NID:g179927; PIDN:AAA35649.1; PID:g179928
A; Nores references: GB:M73499; NID:g179927; PIDN:AAA35649.1; PID:g179928
A; Nore: parts of this sequence, including the amino end of the mature protein, were conf:
R; Long, R.M.; Calabrese, M.R.; Martin, B.M.; Pohl, L.R.
A; Life Scil. 48, PL43-PL49, 1991
A; Title: Cloning and sequencing of a human liver carboxylesterase isoenzyme.
A; Reference number: JH0327; MUID:91148424; PXID:1997784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA; DNA
A;Residues: 1-3,'PALV',8-11,'A',13-567 <SHI>
A;Cross-references: GB:D21088; NID:g455476; PIDN:BAA04650.1; PID:g458470
A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correspond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carboxylesterase (EC 3.1.1.1) precursor, monocyte/macrophage [validated] - human NyAlternate names: carboxylesterase, hepatic; monocyte/macrophage serine esterase (Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A41010; J40327; J47376; A49816; PS0220; IG1085; A48809; IS7004
R;Munger, J.S.; Shi, G.P.; Mark, E.A.; Chin, D.T.; Gerard, C.; Chapman, H.A.
J; Itle: A serine esterase released by human alveolar macrophages is closely related A;Reference number: A41010; MUID:92011649; PMID:1918003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: A47376
Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 61-567 <LON>
A; Cross-references: GB:M55509; NID:g179929; PIDN:AAA35650.1; PID:g179930
A; Cross-references: GB:M55509; NID:g179929; PIDN:AAA35650.1; PID:g179930
G; Shibate, F.; Takagi, Y.; Kitajima, M.; Kuroda, T.; Omura, T.
G; Gromics 17, 76-82, 1993
A; Title: Molecular cloning and characterization of a human carboxylesterase gene.
A; Reference number: A47376; MUID:94010913; PMID:8406473
                                                                                                               58 PPLGSLRFAPPQPAEPWNFVKNTTSYPPMCSQDAVGGQVLSELFTNRKENIPLQFSEDCL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381 LPYIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRM 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPFLKDGASEBETINLSKAVMKYWANFARNGSPNGGGLPHWPEYDQKEGYLKIGASTQAAQ 535
                                                                                                                                                                                                                                                                                                                                          201 LSTDDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLAS 260
                                                                                                                                                                                                                                                                                                                                                                                                           178 FSTGDEHSRGNWGHLDQVAALHWVQDNIANFGGNPGSVTIFGESAGGFSVSALVLSPLAK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLFHRAISOSGTALFRLFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVS 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 NKMRFLQLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 MDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHHARGI-IVKPRTDGADHGDEMYFLFG 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPFATGLSMGKEKALSLOMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLOLDFTTRVGM 559
6 LVW----LFLAACTAWGYPSSPPVVNTVKGKVLGKYVNLEGFAQ-----PVAVFLGIPFAK 57
                                                                                                                                                                                                         141 YLNVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGF
                                                                                                                                                                                                                                             KLKEKKMAFWMSLYQSQRPEK 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :||:|||| | : ||:
536 RLKDKEVAFWSELRAKEAAEE 556
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A;Residues: 1-565 <ROB1->
A;CrossireErences: EMBL:X51974
A;Note: 168-Gln, 247-Lys, 423-Met, and 506-Asn were also found
A;Note: the sequence from Pig. 4 is inconsistent with that from Fig. 5 in having 265-Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X51974; NID:956898; PIDN:CAA36236.1; PID:956899
R;Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A.
Arch. Blochem. Blochem. 495-512, 1994
A;Title: Purification and characterization of two rat liver microsomal carboxylesterases
A;Reference number: S51202; MUID:95077430; PMID:7986098
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A;Residues: 19-26, 70', 28-37 <GAU>
C;Superfamily: cholinesterase; cholinesterase homology
C;Superfamily: cholinesterase; cholinesterase homology
F;1-18/Domain: signal sequence #status predicted <SIG>
F;1-18/Domain: signal sequence #status predicted <AIG>
F;19-565/Froduct: carboxylesterase #status predicted <MAT>
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A,Reaidues: 19-48 eMOR>
R,Medda, S.; Froia, R.L.
Eur. J. Biochem. 206, 801-806, 1992
A,Title: The carboxylesterase family exhibits C-terminal sequence diversity reflecting
A,Reference number: $23460; MUID:92299008; PMID:1606962
A,Accession: $23460
                                                                                                                                                                                                                                                                                                                                                                                                                                        carboxylesterase (EC 3.1.1.1) ES-10 precursor, microsomal - rat
carboxylesterase (EC 3.1.1.1) ES-10 precursor, microsomal - rat
carboxylesterase hydrolase A
carboxylesterase hydrolase A
carboxylesterase hydrolase A
carboxylesterase hydrolase A
carboxylesterase norvegicus (Norway rat)
carboxylesterase 103647, 82468; 551202, 823460; 814361
carboxylesterase number 103647, MUD:90351366; PMID:2386485
A;Reference number: S10367; MUD:90351366; PMID:2386485
A;Reference number: S10367; MUD:90351366; PMID:2386485
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                                                                                                        GGPFATGLSMGKEKALSLQMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLQLDFTTRVG 558
                                                                                                                                            A; Molecule fype: mRNA
A; Readudes: 1-185, 0', 187-422, M', 424-505, M', 507-565 < MED>
A; Readudes: 1-185, 0', 187-42596; MDD: 957553; PIDN: CAA46391.1; PID: 957554
A; Gaustad, R.; Sletten, K.; Lovhaug, D.; Fonnum, F.
Biochem, J. 274, 693-697, 1991
A; Ricle: Purification and characterization of carboxylesterases from rat. lung.
A; Reference number: S14361; MUID: 91190080; PMID: 2012599
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   28 LCWSLTLCLMAQTALG-----ALHTKRPQVVTXYGTLQGKQMHVGKTPIQVFLGVPFSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;50-551/Domain: cholinesterase homology <CHE>F;79,489/Binding site: carbohydrate (Asn) (covalent) #status predicted F;221,466/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, February 1990
A;Reference number: $12468
A;Accession: $12468
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                                                                                                                                                                                                                                                                                        KKLKERKMEFWWQLTEQIMSDRRRK 553
                                                                                                                                                                                                                                                559 MKLKEKKMAFWMSLYQSQRPEKQRQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-264,'K', 266-565 <ROB2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S51202
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Best Local S
Matches 240
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A.Mccession: 819307
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: protein
A.Accession: 823607
A.Accession: 823607
A.Molecule type: protein
A.Accession: 823607
A.Molecule type: protein
A.Accession: 833607
A.Molecule type: protein
A.Mote: 28-1ys and 33-leu were also found
A.Mote: 28-1ys and 33-leu were also found
C.Superfamily: cholinesterase; cholinesterase homology
C.Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer
F.1-18/Domain: signal sequence #status predicted <8IG>
F.1-18/Domain: cholinesterase #status experimental <WAT>
F.51-552/Domain: cholinesterase homology <CREP
F.51-552/Domain: cholinesterase homology carboxyleneral
F.51-522/Acrive site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.; Tsukada, S.; Miki, K.; Kurokawa, K.; Takahas!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of porcine liver proline-beta-:
             439
                                                                                                                  498
                                                                                                                                           GGPFATGLSMGKEKALSLQMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLQLDFTTRVG 558
                                                                                                                                                                                                                                                   140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carboxylesterase (EC 3.1.1.1) precursor - pig
NyAlternate names: proline-beta-naphthylamidase
CiSpecies: Sus scrofa domestica (domestic pig)
CiSpecies: O4-bec-1992 #sequence_revision 04-bec-1992 #text_change 18-Jun-1999
CiAccession: S19307; S23607
Rimatsushims, M.; Inoue, H.; Ichinose, M.; Tsukada, S.; Miki, K.; Kurckawa, FEBS Lett. 293, 37-41, 1991
A;Title: The nucleotide and deduced amino acid sequences of porcine liver professions number: S19307; MUID:92070571; PMID:1959668
        LP-YIMKFPLNRQAMRKETITKMLWSTRTLLNITKBOVPLVVEEYLDNVNEHDWKMLRNR
                                         359 IPMQLMSYPLSEGQLDQXTAMSLLWKSYPLVCIAKELIPEATEKYLGGTD--DTVKKKDL
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                                                                                                               MMDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHH-ARGIIVKPRTDGADHGDEMYFLF
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44.2%; Pred. No. 2e-92;
tive 110; Mismatches 19
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A; Residues: 114 'H', 116-280, 'A', 282-300, 'IGNSYLWTYRETQREST', 318-336,'R', 338-382,'GSPI', 3
A; Cross-references: GBM65261; NID: g187028; PIDN: AAA83932.1; PID: g187029
A; Experimental source: liver
A; Note: differences between this sequence and other reports appear to be due to frameshis references under: lower
A; Note: differences between this sequence and other reports appear to be due to frameshis references under: lower
A; Note: differences between this sequence and other reports appear to be due to frameshis references under: lower, Gonzalez, F.J.
B; Cochemistry 32, 11606-11617, 1933
A; Title: Glycosylation-dependent activity of baculovirus-expressed human liver carboxyle
A; Recence number: A48809; MUID: 94032283; PMID: 8228
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-55, 'G', 57-361, 363-535, 'G', 537-567 <KRO1>
A; Cross-references: GB: LO7765; NID: g180949; PIDN: AAA35711.1; PID: g180948
A; Cross-references: GB: LO7764; NID: g180947; PIDN: AAA16036.1; PID: g180948
C; Genetics:
A; Genetics: GDB: CSS1; HMS
                      lood 78, 506-512, 1991
.ifitle: cDNA cloning and characterization of human monocyte/macrophage serine esterase-Reference number: A49816; MUID:91300111; PMID:2070086
     н.с.
                                                                                              A; Accession: A49816
A; Molecule type: mRNA
A; Cases-references: GB: X52973; NID: 936421; PIDN: CAA37147.1; PID: 91335304
B; Riddles, P.W.; Richards, L.J.; Bowles, M.R.; Pond, S.M.
A; Riddles, P.W.; Richards, L.J.; Bowles, M.R.; Pond, S.M.
A; Title: Cloning and analysis of a cDNA encoding a human liver carboxylesterase.
A; Reference number: PS0280; MUID: 92084150; PMID: 1748313
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     M.R.; Radzun,
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F;564-567/Region: endoplasmic reticulum retention signal #status atypical
F;221,468/Active site: Ser, His #status predicted
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A;Gene: GDB:CES1; HMSE
A;Gene: GDB:128044; OMIM:114835
A;Gene: GDB:13-16422.1
A;Hap position: 1643-16421.1
G;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; liver
F;1-18f/Domain: signal sequence #status predicted <SIG>F;19-145f/Domain: propeptide #status predicted <PRO>F;50-553/Domain: cholinesterase homology cHEs
F;145-553/Domain: cholinesterase homology cHEs
F;146-567/Product: carboxylesterase #status experimental <MAT>
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Buck, F.; Parwaresch,
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Best Local Similarity 44.2%; Pred. No. 2.3e-93;
Matches 250; Conservative III; Mismatches 192;
н.
Salmassi, A.; Kreipe,
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Db 359 LPTWMGFPLSEGKLDQKTATSLLWKSYPIANIPEELTPVATDKYLGGTDDPVKKKDLF 416 Qy 441 MDIVQDATPVYATLQTAHYHRDAGLPVYLXEFEHH-ARGIIVKPRTDGADHGDEMYFLFG 499 11:	TRESHIF 5 Carboxylesterase (EC 3.11.11) ES-3 prequency - rat Carboxylesterase (EC 3.11.11) ES-3 prequency - rat Caperer (Species Ratus norvegicus (Norway rat) R. Redalay (R. R. R. Commun. 20. 1404.1411 1994 A. Filter (Including and sequencing of rat liver (Species ES-3 (EGASYN)) A. Residuant (Cata) (MID-195031008) PHID:194237 A. Residuant (Cata) (Cata) (Cata) (Cata) (Cata) (Cata) A. Residuant (Cata) (C

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Sarboxylesterase (EC 3.1.1.1) ES-4 precursor, liver - rat
Carboxylesterase (EC 3.1.1.1) ES-4 precursor, liver - rat
NiAlterante names: hydrolase B
C.Species Rattus norvegicus (Norway rat)
C.Date: 28-Oct: 1996 Headquence revision 13-Mar-1997 #text_change 18-Jun-1999
C.Accession: S62788; 551203; Ä55304; 54927
E.Robbi, M.; van Schaftingen. E.; Beaulay, H.
Biochem. U. 313, 821-826, 1956
A.Fittle: Cloning and sequencing of rat liver carboxylesterase ES-4 (microsomal palmitoy)
A.Roccession: S62788; MUD:96190723; PMID:8611161
A.Roccession: S62788; MUD:96190723; PMID:8611161
A.Roccession: S62788; MUD:96190723; PMID:8611161
A.Roccession: S62788; MUD:95107430; PMID:7986098
A.Roccession: S62788; MUD:95077430; PMID:7986098
A.Roccession: S5103
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A.Roccession: S5103
A.Roccession: S63788
A.Roccession: S6388-2699; 1994
A.Roccession: S6388-2699; 1994
A.Roccession: S6388-2699
A.Roccession: S6388-2
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                                476 APILRDGASEBEIKLSKAVAMKFWANFARNGNPNARGLPHWPQYDQKEEYLQIGATTQQSQ 535
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                                                                                                                  500 GPFATGLSMGKEKALSLOMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLOLDFTTRVGM
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A;Molecule type: mRNA
A;Residues: 1-561 «802»
A;Cross-references: EMBL:X81825; NID:g550417; PIDN:CAA57419.1; PID:g550418
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Pred. No. 5.6e-88;
3; Mismatches 191; Indels 13;
                                                                                                                                                                                                                                            560 KLKEKKMAFWMSLYQSQRPE 579
                                                                                                                                                                                                                                                                                :|| :::||| | ::|:
536 RLKAEEVAFWTQLLAKRQPQ 555
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Best Local Similarity 41.7%; Pre
Matches 234; Conservative 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic anion (Superfamily: cholinesterase; cholinesterase homology (C; Superfamily: cholinesterase; cholinesterase homology (C; Superfamily: cholinesterase; carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver F; 11-18/Domain: signal sequence #status predicted <SIG.>
F; 19-561/Product: carboxylesterase homology cGFR>
F; 50-551/Domain: cholinesterase homology cGFR>
F; 50-551/Domain: endoplasmic reticulum retention signal F; 79, 301/Binding site: carbohydrate (Asn) (covalent) #status predicted F; 221, 466/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cipecies: Rattus norvegicus (Norway rat)
CiDate: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Sep-1998
CiDate: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Sep-1998
CiAccession: 871597
Rivan, B.; Yang, D.; Parkinson, A.
Arch. Biochem. Biophys. 317, 222-234, 1995
A;Title: Cloning and expression of hydrolase C, a member of the rat carboxylesterase in A;Reference number: 871597; MUID:95177656; PMID:7872788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 GLFHRAISQSGTALFRIFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVS 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 NYMRFLOLNFORDPEELIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 MRWILCWSLTLCLMA--QTALGALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPFSR 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57
                                                       KDQLELIGDVVFGVPSVIVSRGHRDAGAPTYMYEFQYSPSFSSEMKPDTVVGDHGDEIY
                                                                                                                                         FLEGGPFATGLSMGKEKALSLQMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLQLDFTT
                                                                                                                                                                                       SVFGAPILRGGTSEEBINLSKWYMKFWANFARNGNPNGQGLPHWPEYDQKEGYLQIGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 PPLGILRFAPPEPPEPWKGIRDATTYPPGCLQESW-GQLASMYVSTRERYKWLRFSEDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 LSTDDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 EXMNLIKISSQRDIKESYHFLSTVIDDVVLPKDEILAEKNFNTVPYIVGINKQECGWL
                      RNRMMDIVQDATFVYATLQTAHYHRDAGLPVYLYBFBHH-ARGIIVKPRTDGADHGDEMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 PPLGSLRFAPPQPAEPWSFVKNTTTYPPMCSQDATKGQRNNDLLTNRKEKVHLQFSEDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLNVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carboxylesterase (EC 3.1.1.1) precursor, liver - rat N,Alternate names: hydrolase C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Experimental source: liver; endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Status: not compared with conceptual translation A,Molecule type: mRNA
A,Residues: 1-561 <YAN>
                                                                                                                                                                                                                                                                   RVGMKLKEKKMAFWMSLY-QSQRPEKQRQ 583
                                                                                                                                                                                                                                                                                                          : ||||||::||| | : | : : : : CQAQKLKEKEVAFWIELLAKKQLPTEHTE 561
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	OY 320 SNKWRFLQINFORDPEEIIWSWSPVUGGVIPDDPLYLL 288 KTEAELELTVKLDNTSWSTVIDGVVLPYEPEBIL OY 380 LLPYIMKPPLNROAMRKETITKMLWSTRTLLNITKEOVE 1	402 499 462 559 523	RESULT 10 Al1584 Carboxylesterase (BC 3.1.1.1) precursor - rat (fragm Carboxylesterase (BC 3.1.1.1) precursor - rat (fragm C) Capter Sattus norvegicus (Norway rat) C;Date: 21-May-1990 #sequence_revision 03-Aug-1992 #C;Accession: A31584	Rilong, R.M.; Sarch, H.; Martin, B.M.; Kimura, S.; Golden. Biochem. Biophys. Res. Commun. 156, 866-873, 1988 A;Title: Rat liver carboxylesterase: cDNA cloning, se A;Reference number: A31584 A;Molecule type: mRNA A;Residues: 1-540 *CLON A;Cross-references: GB:MZ0629; GB:X13587; NID:g203275 C;Superfamily: cholinesterase; cholinesterase homolog C;Keywords: carboxylesterase; spredicted *S1-9,Doroduct: carboxylesterase whomolog C;Keywords: carboxylesterase homolog C;Keywords: carboxylesterase homolog C;F;10-540/product: carboxylesterase homolog F;10-540/product: carboxylesterase homology CHE> F;212,444/Active site: Ser, His #status predicted F;212,444/Active site: Ser, His #status predicted CHE> Best Local Similarity 43.8%; Pred. No. 4e-85; Matches 237; Conservative 96; Mismatches 188; Matches 237; Conservative 96; Mismatches 188; CD NO NTTYPPPMCSQDGVVGKLLADMLSTGKESIPLEFSEDCI CONSERVACHGRAVSIEGFTOPVAVELCVPFARM CON 103 DATTYPPPMCSQDGVVGKLLADMLSTGKESIPLEFSEDCI CONSERVACHGASSYPGGABANETSGLMWSPLARE CONSERVACHGASPARE CONSERVACHGRALSAHENVVVVVDCHRIGTEGFGGD CONSERVACHGASPYRGGABANETSGLMWSPLARE CONSERVACHGASPASCHANSTGLMAREACHARE CONSERVACHGASPARE CONSERVACHARGGNPORVITEGESAGGSVSALVISPERATOR CONSERVACHARGGNPORVITEGESAGGSVSALVISPERATOR CONSERVACHARGGNPORVITEGESAGGSVSALVISPERATOR CONSERVACHARGGNPORVITEGESAGGSVSALVISPERATOR CONSERVACHARGANDRATEGENPORVACHARGANDRATEGENPARE CONSERVACHARGANDRATEGENPARE CONSERVACHARG
	Db 178 FSTGDEHSRUNWGHLDQVAALHWVQDNIANFGGDPGSVTIFGESÄGGFSVSVLVLSPLTK 237 Qy 261 GLFHRAISQSGTALFRLFITSNPLKVAKKVAHLAGCNHNSTOILVNCLRALSGTKVMRVS 320 238 NLFHRAISGSGTALFREFITSNPLKVAKKVAHLAGCNHNSTOILVNCLRALSGTKVMRVS 320 Qy 321 NKWRFLQLNFQRDPEEIIWSMSPVVDGVVIPDDFLVLTGGKVSSVPYLLGVNNLFFNWL 380 Db 298 KKWALIKLSSORDNKESXYHFLSTVVNNVLFKDPKEILAEKNFWPYVVPYVVOKCWM. 357	381 381 440 415 499		RESULT 9 JAX0054 Carboxylesterase (EC 3.1.1.1) El precursor, minor form - rat Carboxylesterase (EC 3.1.1.1) El precursor, minor form - rat Carboxylesterase (EC 3.1.1.1) El precursor, minor form - rat Carboxylesterase (BC 3.1.1.1) El precursor, minor form - rat Carboxylesterase (BC 3.1.1.1) El branche (Boxway rat) Carbox 120054 R. Takagi, Y.; Morchashi, K.; Kawabata, S.; Go, M.; Omura, T. J. Biochem 104, 801-805 1988 A; Reference number: JAX0054; MulD:80174514; PMID:3235453 A; Reference number: JAX0054; MulD:80174514; PMID:3235453 A; Reference number: JAX0054 A; Molecula type: MRNA A; Repeimental Source: liver C; Superfamily: cholinesterase; cholinesterase blacked to Side (Side Family) A; Repeimental source: liver C; Superfamily: cholinesterase Blacked to Side (Side Family) A; Reportmental source: liver C; Superfamily: carboxyleterase Blacked to Side (Side Family) A; Reportmental source: liver C; Superfamily: carboxyleterase Blacked to Side (Side Family) A; Reportmental source: liver C; Superfamily: carboxyleterase Blacked to Side (Side Family) A; Reportmental source: liver C; Superfamily: carboxyleterase Blacked to Side (Side Marches) F; 1-18/Domain: signal sequence #status predicted carboxyleterase Blacked to Side (Side Marches) F; 1-18/Domain: cholinesterase Blacked to Side (Side Marches) Bost Local Similarity A; 5-6-6-6-6-6-6-6-6-6-6-6-6-6-6-6-6-6-6-6

sequencing, and evidence for a multigg 3315 (Asn) (covalent) #status predicted 79; PIDN:AAA40871.1; PID:g203280 ogy LLTQGKVSSVPYLLGVNNLEFNW 379 :||: ::|||::| | | | ILTEKSFNTVPYIVGFNKQEFGW 343 CLYINVYAPARAPGDPQLPVMVW 161 GFLSTDDSHARGNWGLLDQMAAL 221 NVTLFGQSAGAMSISGLMMSPLA 259 NHNSTQILVNCLRALSGTKVMRV 319 |: |: | | | | | NNTSSAAMVQCLRQ----- 287 VPLVVEEYLDNVNEHDWKMLRNR 439
:| ::|:|| ::|
IPAIIEKYLRGTDDPAKK--KEL 401 LPCWPRYNKDBKYLQLDFTTRVG 558 SRPPLGILRFAPPEPPEPWKGIR 102 ASGLFHRALSQSGTALFRLFITS 281 | |||||||:|| AKNLFHRAISESGVVLTINLDKK 249 VSNKMRFLQLNFQRDPEEIIWSM 341 || || ||::| |||: LPHWPEYDQKEGYLQIGATTQQA 521 Gonzalez, F.J.; Pohl, L.R. #text_change 18-Jun-1999 8; Indels 20; Gaps ; Length 540; d <MAT>

QQ		qa	346 IIPWALQNLLPEGKWNETASLLLRRFHSELNISESMIPAVIEQYLRGVDDPAKKSEL 403
\$ 6	342 SPVVDGVVIPDDPLVLITQGKVSSVPYLLGVNNLEFNWLLPYIMKFPLNRQAMRKETITK 401 - - - -	δ, 62	440 MMDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHHARGIIVK-PRIDGADHGDEMYFLF 498 :: :
کې م م	402 MLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRWMDIVQDATFVYATLQTAHYHR 461 	\$ 6 6	499 GGPFATGLSMGKEKALSLOMMKYWANFARTGNPNDGNLFCWPRYNKDEKYLQLDFTTRVG 558
දු අ	462 DAGLPVXLYEFEHHARGII-VKPRTDGADHGDEMYFLFGGPFATGLSMGKEKALSLQMMK 520	, & 43	S59 MKLKEKKNAFWASLYQSQRPE S79
6 6 6	521 YWANFARTGNPNDGNLPCWPRYNKDEKYLQLDFTTRVGMKLKEKKNAFWMSLYQSQRPEK 580 :	RESULT 12	
ò i	Q 581	carboxyle C;Species C;Date: 0	sterase (EC 3.1.1.1), TCCD-induced 60K microsomal - rabbit: Oryctolagus cuniculus (domestic rabbit) 3-Dec-1988 #sequence revision 08-Dec-1988 #text change 21-Aug-1998
RESULT		C, Accessi R, Korza, J. Biol. A:Title:	on: A28923; A29471 3.; Ozols, J. Amm. 263, 3486-3495, 1988 Complete covalent structure of 60-kDa esterase isolated from 2.3.7 8-tetrachlo
A39060 carboxy C;Speci	.1999	A; Referen A; Accessi A; Molecul A; Residue	
C; Acces R; Ovnic Genomic:	Grant, S.G.; Gan	R;OZOLS, J. Biol. A;Title:	J. Them. 262, 15316-15321, 1987 Isolation and characterization of a 60-kilodalton glycoprotein esterase from l
A;Refer A;Acces	DOXYIESCEIGSE IIIL	A; Kereren A; Accessi A; Molecul	se numoer: Azy4/1; MULD:88U331Z4; FMLD:356/634 on: AZ9471 e type: brotein
A; Statu A; Molec A; Residu A; Cross C; Superi C; Keywol	A,Status: preliminary A;Molecule type: mRNA A;Residues: 1-554 <0VN> A;Residues: 1-554 <0VN> C;Superferences: GB:N57960; NID:g192853; PIDN:AAA63297.1; PID:g192854 C;Superfamily: cholinesterase; cholinesterase homology C;Reywords: carboxylic ester hydrolase	A, Residue C, Superfa C, Keyword F, 32-526/ F, 61, 363/ F, 195, 441	A; Residues: 1-71,193-208; 436-446; 532-539 <020> C; Superfamily: cholinesterase; cholinesterase homology C; Superfamily: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein F; 32-55/ Domain: cholinesterase homology <che> F; 52-55/ Domain: cholinesterase homology <che> F; 61,363/ Binding site: carbohydrate (Asn) (covalent) #status experimental F; 195,441/ Active site: Ser, His #status experimental</che></che>
F; 221, 4.		Query Match Best Local	7
Best : Match	Local Similarity 41.5%; Pred. No. 1.78-84; Matches 233; Conservative 113; Mismatches 190; Indels 25; Gaps 10;	Macches	22/; Conservative 115; Mismacches 1//; Indels 30; Gaps 10; 46 HTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPFSRPPIGILRFAPPEPPEP 97
ठे ह	WILCW-SLTLC-LMAQTAL-GALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPFS	Dp	
g &	2 WLHALVWASLAVCPILGHBILPPVVDITQGKVLGKYISLEGFEQPVAVFLGVPFA 56 81 RPPLGILRFAPPEPPPWKGIRDATTYPPGCLQES-WGQLASMYVGTRERYKWLRFSEDC 139	ò a	98 WKGIRDATTYPPGCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQ 155
да .:	YPPLGSLRFAPPQPAEPWSFVKNATSYPPMCSQDAGWAKILSDMFSTEKEILPLKISEDC 11.	Å :	LPVMVWFPGGAFIVGAASSYEGSDLAAREKVYLVFLOHRLGIFGFLSTDDSHARGNWGLL
B vá	140 DYLNVYARAKAPUDPQLPYNVWFFGGAFIVGAASSYEGSDLAAREKVVLVFLQHRIGIFG 199 	g &	115 LPVMVWIHGGGLMVGGASTYDGLALSAHENVVVVTIQYRLGIGGFGFNIDEL 166 216 DQWAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLWMSPLASGLFHRAISQSGTALF 275
જે દે	200 FLSTDDSHARGNWGLLDQMAALRWVQENTAAFGGDFGNVTLFGQSAGAMSISGLMMSPLA 259	ସ୍ପ :	:
8 8		λό da	276 KLFITSNPLKYAKKVAHJAGCNHNSTQILVNCLRALSGIKVMRYSNKMRELQLNFGRDPE 335 227 SSLFRKNIKSLAEKIAIBAGCKTTTSAVAVHCLRQKTEBELMEVTLKMKFMALDLVGDPK 286
요 &	SGVVINTNVGKKNIQAVNEIIATL FORDPERITWSMSPVVNGVVIPDD	ð : £	336 BIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNNLLP-YIMKFPLNRQAM 394
7 da 6	: :	ි ර යි	RKETITKALMSTRILLMITKEQVPLVVBEXLDNVNEHDWKMLRNRMMDIVQDATFVDATL
ì		;	

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carboxylesterase (EC 3.1.1.1) precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 20-Jun-2000
C;Accession: S47655
R;Sone, T.; Isobe, M.; Takabatake, E.; Wang, C.Y.
Biochim. Babophs. Acta 1207, 138-142, 1994
A;Title: Cloning and sequence analysis of a hamster liver cDNA encoding a novel putative A;Reference number: S47655, MUID:94318665; PMID:8043605
A;Recession: S47655
A;Accession: S47655
A;Accession: S47655
A;Accession: S47655
A;Coss-references: EMBL:D28566; NID:g531238; PIDN:BAA05913.1; PID:g531239
C;Superfamily: cholinesterase; homology
C;Keywords: carboxylic ester hydrolase
F;S8-546/Domain: cholinesterase homology cCHE>
F;227,459/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258
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CLYLNVYAPARAPGDPQLPVM/WFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIF 198
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                                                                      GGPFATGLSMGKEKALSLOMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLQLDFTTRVG 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 VGPLRFAPPEPPEPWSGVRDGTSEPAMCLQTDFMRPQI-----SKERKIILPTISMSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 ASGLEHRAISQSGTALFRIFITSNPLKV-AKKVAHLAGCNHNSTQILVNCLRALSGTKVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 SKGLFHGAIMÓSGVALLPDLISDTPEAVYTPVVANQSGCEAKDSEALVHCLREKTEAEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 RVSNKMRFLQLNFQRDPEEIIWSMSP-VVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 CGWGVPLFWGLDHVIKNITRETLPAFLKSRAEHWMLPPECSDLLMQEYMGDV--EDPQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CWSLTLCLMAQTALGALH---TKRPQVVTKYGTLQGKQMHV--GKTPIQVFLGVPFSRPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNRMMDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHHARGI---IVKPRTDGADHGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           377 FNWLLPYIMKFPLNRQAMRKETITNWLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWRML
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34.1%; Score 1060; DB 2; Length 56

Best Local Similarity 41.1%; Pred. No. 7.1e-78;

Matches 234; Conservative 97; Mismatches 191; Indels
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A.Experimental source: intestine
C.Comment: This enzyme hydrolyzes many xenobiotics, such as carboxyl esters, thioesters
C.Comment: This enzyme hydrolyzes many xenobiotics, such as carboxyl esters, thioesters
C.Genetics:
A.Gene: GB:CES2; ICE; CE2
A.Gene: GB:CES2; ICE; CE2
C.Superimental: C.Superimenters: GB:S958911
C.Superimental: C.Superimenters: GB:S958911
C.Superimental: C.Superimenters: GB:S95891
C.Superimental: GB:CES2
C.Superimental: C.Superimenters: GB:S95891
C.Superimental: GB:CES3
C.Superi
                                                                                                                                                                                                                                                                                                                                                                                         carboxylesterase (EC 3.1.1.1) - human
C;Species: Homo sapiens (man)
C;Species: 10-69p-1999 #sequence_revision 10-8ep-1999 #text_change 16-Jun-2000
C;Accession: JC5408
R;Schwer, H; Langmann, T; Daig, R; Becker, A; Aslanidis, C; Schmitz, G.
Biochem, Biophys. Res. Commun. 233, 117-120, 1997
A;Title: Molecular cloning and characterization of a novel putative carboxylesterase, A;Reference number: JC5408; MUID:97289502; PMID:914407
                                                         573
                                                                                                                                                             GILRFAPPEPPEPWKGIRDATTYPPGCLOESWGQLASMYVSTRERYKWLRFSEDCLYLNV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPLRFAPPEPPESWSGVRDGTTHPAMCLQDLTAVESEFLSQFNMTFPSDSMSEDCLYLSI 128
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                               QTAHYHRDAGLPVYLYEFEHH-ARGIIVKPRTDGADHGDEMYFLFGGPFATGLSMGKEKA 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 ILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMHV--GKTPIQVFLGVPFSRPPL
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40.8%; Pred. No. 9.6e-80;
tive 94; Mismatches 204;
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232; Conserv
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A;Molecule type: mRNA
A;Residues: 1-559' <SCH>
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us-10-001-227-2.rpr
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Sydoxylesterase (EC 3.1.1.1) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: Syd607
R;Aida, K; Moore, R; Negishi, M.
Biochim. Biochim. Biophys. Acta 1174, 72-74, 1993
A;Title: Cloning and nucleotide sequence of a novel, male-predominant carboxylesterase is A;Reference number: S34607, MUID:93326638; PMID:7916639
A;Tatus: preliminary
A;Molecule type: mRND
A;Status: preliminary
A;Molecule type: mRND
A;Cross-references: GB:S64130; NID:9404388; PIDN:AAB27606.1; PID:9404389
C;Superfamily: cholinesterase; cholinesterase homology
C;Superfamily: cholinesterase; homology cHE>
F;46-536/Domain: cholinesterase homology cHE>
F;215,443/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 FVYATLOTAHYHRDAGLPVXLXEFEHHARGII-VXPRTDGADHGDEMYFLFGGPFATGLS 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 LVIPTLIFSKYLQDAGCPVFLYEFQHTPSSFAKFKPAWVKADHSSENAFVFGGPFLTDES 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 PLPPQPWEGVRDASINPPMCLQDV-ERMSNSRFTLNEKWKIFPISEDCLTLNIYSPTEIT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 GDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGN 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 WGLLDQMAALRWYQENIAAFGGDPGNYTLFGQSAGAMSISGLMMSPLASGLFHRAISQSG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 RGFLDVVAALRWVQGNIAPFGGDPNCVTIFGNSAGGIIVSSLLLSPMSAGLFHRAISQSG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 TALFRLFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQ 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 VVISKILEDINAWSEAQNFANSVACGSASPAELVQCLLQKEGKDLITKKNV----- 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 RDPREIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPYIMKFPLNR 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 LCLMAQTALGALHTKRPQVVTKYGTLGGKQMHVGKTP--IQVFLGVPFSRPPLGILRFAP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 QAMRKETITKMLWSTRTLL---NITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDAT
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 554;
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Best Local Similarity 41.1%; Pred. No. 9e-76;
Matches 232; Conservative 89; Mismatches 205; Indels
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Search completed: August 3, 2004, 22:28:52 Job time : 23 secs

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August 3, 2004, 22:24:36 ; Search time 13 Seconds (without alignments) 2339:152 Million cell updates/sec
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3112
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Perfect score:
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141681 Total number of hits satisfying chosen parameters:

141681 segs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                                                          VYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLST 203
                                                                                                                                             DDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLF 263
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                                                                                                                                                                                                               324 RFLQLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPY 383
                                                                                                                                                                                                                                                  384 IMKFPLNRQAMRKETITKMLWSTRTL--LNITKEQVPLVVEEYLDNVNEHDWKMLRNRMM 441
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                                                               84
                                                                      GILRFAPPEPPEPWKGIRDATTYPPGCLQES-WGQLASMYVSTRERYKWLRFSEDCLYLN
                                                            27 ILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMHV--GKTPIQVFLGVPFSRPPL
                                                                                                                                                                                                                                                                                                                        DIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHH---ARGIIVKPRTDGADHGDEMYFLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley, and Wistar; TISSUE=Liver;
MEDLINE=90351366; PubMed=2386485;
Robbi M., Beaufay H., Octave J.-N.;
"Nucleotide sequence of cDNA coding for rat liver pI 6.1 esterase
(ES-10), a carboxylesterase located in the lumen of the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                            ESIO RAT STANDARD; PRT; 565 AA.
P16303; Q64574;
P16303; Q64574;
P16303; Q64574;
P16300 (Rel. 15, Created)
O1-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Liver carboxylesterase 10 precursor (EC 3.1.1.1) (Carboxyesterase 10) (PI 6.1 esterase)
476 476 N-LINKED (GLCNAC. . .) (POTENTIAL)
557 AA, 61637 MW, 03E35D90A037F6B0 CRC64;
                                            27;
                           Length 557;
                        ore 1290.5; DB 1; Length ed. No. 4.8e-95; Mismatches 172; Indels
                          41.5%; Score 1290.5;
46.0%; Pred. No. 4.8e
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529 KKLKERKMEFWMQLTEQIMSDRRRK 553
                                                                                                                                                                                                                                                                                                                                                                                 559 MKLKEKKMAFWMSLYQSQRPEKORQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE=Liver;
                                           Conservative 106;
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                                  Similarity
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                       Query Match
Best Local Simil
Matches 260; C
CARBOHYD
SEQUENCE
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                       Medda S., Proia R.L.;
"The carboxylesterase family exhibits C-terminal sequence diversity
refibering the presence or absence of endoplasmic-reticulum-retention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIVER CARBOXYLESTERASE 10.

BY SIMILARITY.

PREVENT SECRETION FROM ER (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

R -> O (IN SPRAGUE-DAMLEY).

K -> N (IN SPRAGUE-DAMLEY).

K -> N (IN SPRAGUE-DAMLEY).

K -> N (IN SPRAGUE-DAMLEY).

S -> N (IN SPRAGUE-DAMLEY).

S -> N (IN SPRAGUE-DAMLEY).

S -> Y (IN REP. 3).

SK -> TQ (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                     carboxylic anion.
-!- SUBUNIT: Homotrimer.
-!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 LCWSLTLCLMAQTALG-----ALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPFSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 YLNVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGF
                                                                                                                                                                                                                                                                                                                           Biochim. Biophys. Acta 1259:305-312(1995).
-!- FUNCTION: PROBABLY INVOLVED IN THE METABOLISM OF XENOBIOTICS AND
OF NATURAL SUBSTRATES.
                                                                                                                                                                                                                                              Ghosh S., Mallonee D.H., Hylemon P.B., Grogan W.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)0 = an alcohol + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR002018; CarbesteraseB.
Interpro; IPR00319; Ser estrs.
Pfam; PF00113; COSEterase; 1.
PR0SITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00411; CARBOXYLESTERASE B 2; 1.
Hydrolase; Serine esterase; Glycoprotein; Endoplasmic reticulum; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 565;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.5%; Score 1259; DB 1; 43.0%; Pred. No. 1.6e-92;
                                                                                                                         Eur. J. Biochem. 206:801-806(1992).
                                                                                                                                                                                                 STRAIN=Sprague-Dawley, TISSUE=Liv
MEDLINE=96130267; Pubmed=8541339;
MEDLINE=92299008; PubMed=1606962;
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273 284
562 565
79 489
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423 506
420 A
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62144 MW; k
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HSSP; P21836; 1MAA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 YLNVYTPADLTKNSRLPVMYWIHGGGLVVGGASTYDGQVLSAHENVVVVTIQYRLGIWGF 177
                                                                   178 FSTGDEHSRGNWGHLDQVAALHWVQDNIANPGGNPGSVTIFGESAGGFSVSALVLSPLAK
                                                                                                                                                238 NLFHRAISESGVVLTSALITTDSKPIAKLIATLSGCKTTTSAVMVHCLRQKTEDELLETS
                                                                                                                                                                                                                                                                                                                       358 IPTLMGYPLSEGKLDQXTAKSLLWKSYPTLKISEKMIPVVAEKYFGGTD--DPAKRKDLF
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TISSUBE-Peripheral blood, and Placenta;
TISSUB-P94010913; PubMed-8406473;
Shibata F., Takagi Y., Kitajima M., Kuroda T., Omura T.;
Molecular cloning and characterization of a human carboxylesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P23141; Q00015; Q13657; Q14062; Q16737; Q16788; Q9ULY2; Q1-NOV-1991 (Rel. 20, Created) Q1-NOV-1991 (Rel. 21, Last sequence update) Q1-AUG-1992 (Rel. 23, Last sequence update) MARA-2004 (Rel. 43, Last annotation update) Liver carboxylesterase precursor (EC 3.1.1.1) (Acyl coenzyme A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine esterase) (HMSE) (Serine esterase 1) (Brain carboxylesterase hBrl). CESI OR CES2 OR SESI.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=92011649; PubMed=1918003;
Munger J.S., Shi G.P., Mark E.A., Chin D.T., Gerard C.,
Chapman H.A.;
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Biochemistry 32:11606-11617(1993).
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MEDLINE-94032283; PubMed-8218228;
Kroetz D.L., McBride O.W., Gonzal
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E. C. Schnic C., Schnic C., Schnic C.,

R. SCHRIC C. Schnic C., Schnic C.,

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               LPHRAISQSGTALFRLFITSNPLK-VAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVS 320
                                                                                                                                                                 GGPFATGLSMGKEKALSLOMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLOLDFTTRVG 558
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                                    321 NKWRFLQLNFQRDPEFIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWL
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                                                                                               LP-YIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNR
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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InterPro; IPR00379; Ser_estrs.
Pfam; PF00135; Coesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsushima M., Inoue H., Ichinose M., Tsukada S., Miki K., Kurokawa K., Takahashi T., Takahashi K.; Matsuncabotide and deduced amino acid sequences of porcine proline-beta-naphthylamidase. Evidence for the identity with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Liver carboxylesterase precursor (EC 3.1.1.1) (Proline-beta-
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HSSP; P21836; 1MAH
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PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B_2; 1.
Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum; Signal; Multigene family; Polymorphism.
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M -> WA (IN REF. 3)

A -> G (IN REF. 7)

B -> H (IN REF. 7)

D -> H (IN REF. 9)

M -> A (IN REF. 9)

W -> A (IN REF. 8)

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S -> N (in dbSNP:2307240).

/FTIG=VAR 014314.

R -> H (in dbSNP:2307243).

/FTIG=VAR 014594.

D -> E (in dbSNP:2307227).
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                                                          PIR; A41010; A41010.

HSSP; P21836; 1MAH.
Genew; HGMC:1863; CES1.
MIM; 114835; -: GO; GO:0004759; F:serine esterase activity; TAS.
GO; GO:0008152; P:metabolism; TAS.
GO; GO:0009535; P:response to toxin; TAS.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR00379; Ser_estrs.
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             EMBL; M55509; AAA35650.1;
EMBL; X52973; CAA37147.1;
EMBL; M65261; AAA83932.1;
EMBL; S73751; AAC60631.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPFATGLSMGKEKALSLQMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLQLDFTTRVGM 559
                                                                                                                                                                                                                                                                                                                                                                                     82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLGILRFAPPEPPEPWKGIRDATTYPPGCLQESWGQ--LASMYVSTRERYKWLRFSEDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSTGDEHSRGNWGHLDQVAALHWVQENIANFGGDPGSVTIFGESAGGESVSVLVLSPLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHH-ARGIIVKPRTDGADHGDEMYFLFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKWRFLQLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWL
                                                                                                                                                                                                                                                                                                                                                                                                                    299 LKMKFLTLDFHGDQRESHPFLPTVVDGVLLPKMPEEILAEKDFNTVPYIVGINKQEFGWL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                    Gaps
                   BY SIMILARITY.
LIVER CARBOXYLESTERASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
PREVENT SECRETION FROM ER (POTENTIAL).
N-LINKED (GLCMAC. . .) (POTENTIAL).
W, BE046545307DEDE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST3 RAT STANDARD; PRT; 561 AA.

063106;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Liver carboxylesterase 3 precursor (EC 3.1.1.1) (Carboxyesterase 1)
(pl 5. esterase) (ES-HTEL)
Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                           Score 1239.5; DB 1; Length
Pred. No. 5.6e-91;
                                                                                                                                                                                                                                                                                                                                  Conservative 110; Mismatches 192; Indels
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SEQUENCE FROM N.A.
SEXEMIN=Sprague-Dawley, TISSUE=Liver;
MEDLINE=95032008; PubMed=7945287;
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RLKGEEVAFWNDLLSKEAAKK 557
                                                                                                                                                                                                                               62016 MW;
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222
467
1117
285
566
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88
274
563
80
566 AA;
                                                                                                                                                                                                                                                                                                            Similarity
Signal; Multigene
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                  Matches 248;
                                                                      ACT_SITE
ACT_SITE
DISULFID
DISULFID
                                                                                                                                                                           SITE
CARBOHYD
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                                                                                                                                                                                                                                                                                                         Local
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EST3 RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
Robbi M., Beaufay H.;
"Cloning and sequencing of rat liver carboxylesterase ES-3 (egasyn).",
Biochem. Biophys. Res. Commun. 203:1404-1411(1994).
-!- FUNCTION: Involved in the detoxification of xenobiotics and in the
activation of ester and amide prodrugs.
-!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 HKAISESGVALTAGLVKKNTRPLAEKIAVVSGCKSTTSASMVHCLRQKTEEELLETTLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GILRFAPPEPPEPWKGIRDATTYPPGCLQES-WGQLASMYVSTRERYKWLRFSEDCLYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GSLRFAPPQPAEPWSFVKNTTSYPPMCSQDPVAGQIVNDLLTNWEENISLQFSEDCLYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYAPARAPGDPQLPVMVWFPGGAPIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LC-WSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMHV-GKT-PIQVFLGVPFSRPPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLF
                                                                                                                                   SIMILARITY: Belongs to the type-B carboxylesterase/lipase family
                                                                                                     -!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.

LIVER CARBOXYLESTERASE 3.

BY SIMILARITY.

BY SECRETION FROM ER (POTENTIAL).

N-LINKED (GLUNAC. .) (POTENTIAL).

N-LINKED (GLUNAC. .) (POTENTIAL).

N-LINKED (GLUNAC. .) (POTENTIAL).

N-LINKED (GLUNAC. .) (POTENTIAL).

M; 1E14D66DF089B86F CRC64;
                                                                                                                                                                                                                                                                                                   PIR; JC2447; JC2447.
HSSP; P21836; IMAA.
InterPro; IPRO002018; CarbesteraseB.
InterPro; IPRO002018; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00141; CARBOXVIESTERASE B 1; 1.
PROSITE; PS00941; CARBOXVIESTERASE B 2; 1.
Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.7%; Score 1205.5; DB 1; Length 561; 43.3%; Pred. No. 2.9e-88; cive 114; Mismatches 191; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW.
                                                                                                                                                                                                                                                                                    EMBL; X81395; CAA57158.1; -. PIR; JC2447; JC2447.
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221
466
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61714 P
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                                                                                          carboxylic anion.
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466
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CARBOHYD
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DISULFID
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61581 MW; FB1A4367A0CCB2E3 CRC64;
                                                        38.7%;
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     562 AA;
                                                                                      Similarity
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Q63010;
                                                        Query Match
Best Local S:
Matches 241
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     SEQUENCE
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                                                                                                                                                    VODATFVYATLOTAHYHRDAGLPVYLYEFEHH-ARGIIVKPRIDGADHGDEMYFLFGGPF 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=92147141; PubMed=1783403;
Ovnic M., Swank R.T., Fletcher C., Zhen L., Novak E.K., Baumann H.,
Heintz N., Ganschow R.E.;
"Characterization and functional expression of a cDNA encoding egasyn (esterase-22): the endoplasmic reticulum-targeting protein of beta-glucuronidase."; per endoplasmic reticulum-targeting protein of beta-Genomics 11:956-967(1991).
--- FNUCTION: Involved in the detoxification of xenobiotics and in the
                                                        IGDVIFGVPSVIVSRGHRDAGARTYMYEFQYRPSFSSKMKPSTVVGDHGDEIYSVFGAPI
                                                                                                                ATGLSMGKEKALSLOMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLQLDFTTRVGMKLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Esterase-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activation of ester and amide prodrugs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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PROSTITE; PS00122; CARBOXYLESTERASE B 1; 1.
GLYCOPITE; PS00941; CARBOXYLESTERASE B 2; 1.
Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum; Signal, Multigene family.
BY SIMILARITY.
CHAIN
20 562 LIVER CARBOXYLESTERASE 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Liver carboxylesterase 22 precursor (RC 3.1.1.1) (Egasyn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carboxylic anion.
SUBCELLULAR LOCATION: Microsomal membrane, lumen of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.

LIVER CARBOXYLESTERASE 22
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
PREVENT SECRETION FROM EF
N-LINKED (GLCNAC. . . ) (INCLINKED (GLCNAC. . . . )
                                                                                                                                                                                                                                                                                                                                                                                                                            562 AA
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PIR; A55281; A55281.
HSSP, P21836; 1MAH.
MGD, MG1:95432; E622.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
                                                                                                                                                                                                                              EKKMAFWMSL 572
                                                                                                                                                                                                                                                                                   EKEVAFWSEL 548
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222
467
1117
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           472
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                                                                                                                             1 MCLSALILVSLAAFTAGAGHPSSPPMV---DTVQGKVL--GKYISLEGFTQPVAVFLGVP
                                                                                       ----TPIQVFLGVP
                                                                                                                                                                                                                                                                                             FGFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSP
                                                                                                                                                                                                                                                                                                                                                                                318 RVSNKMRFLQLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 GTTLKINLFKLDLHGDSRQSHPFVPTVLDGVLLPKMPEEILAEKNFNTVPYIVGINKQEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NWILLPYIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWK-ML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   437 RNRWMDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHH-ARGIIVKPRTDGADHGDEMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           496 FLFGGPFATGLSMGKEKALSLQMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLQLDFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVFGAPILRGGTSEEEINLSKAMMKFWANFARNGNPNGQGLPHWPEYDQKEGYLQIGATT
                                                                                                                                                                                                                                                                      DCLYLNVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGI
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                            Gaps
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Liver carboxylesterase B-1 precursor (EC 3.1.1.1) (Liver microsomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activation of ester and amide prodrugs.
-!- CATALTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a carboxylic anion.
-!- SUBCELLUIAR LOCATION: Microsomal membrane, lumen of endoplasmic
                                          21;
  DB 1; Length 562;
                                          Conservative 119; Mismatches 188; Indels
                                                                                       28 LCWS-LTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMHVGK-
Score 1205.5; DB Pred. No. 2.9e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ā
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                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 NKWRFLQLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWL 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAFIGDVLFCIPSVMVSRDHRDAGAPTÝVÝEYQYYPSFSSPQRPKDVVGDHADDVÝSVFG 475
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                              SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.

LIVER CARBOXYLESTERASE B-1.

BY SIMILARITY.

PREVENTION FROM ER (POTENTIAL).
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InterPro; ITRO02018; Extraget_S.
InterPro; IPR000379; Setrs
Pfam; PP00115; Costerase; 1.
PROSITE; PS00014; Extragar; 1.
PROSITE; PS000941; CARBOXVLESTERASE_B_1; 1.
PROSITE; PS00941; CARBOXVLESTERASE_B_2; 1.
Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum; Signal; Multigne family.
Signal; Multigne family.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 561;
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013C1C13ACEBC6C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 123; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.2%; Score 1187.5; DB 41.1%; Pred. No. 7.8e-87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62494 MW;
                                                                                                                                                                                                                                                                                                                                             EMBL; U10698; AAA64639.1; -.
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221
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                                                                                                                                                                                             (Carboxyesterase ES-4)
                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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MEDLINE=S050819; PubMed=7961958;
Wan B., Yang D., Brady M., Parkinson A.;
"Rat kidney carboxylesterase. Cloning, sequencing, cellular localization, and relationship to rat liver hydrolase.";
J. Biol. Chem. 269:29688-29696(1994).
I- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND ACTIVATION OF ESTER AND ANDE PRODRUGS. HYDROLYZES OMICRON-NITROPHENYL ACETATE AND ALPHA-NAPHTHYL ACETATE. IT ALSO NITROPERNYL ACETATE AND DISTINCTIVELY, PAINATIONI-COA.
I- CAMALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol
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InterPro; IPRO12018; CarbesteraseB.
InterPro; IPRO12018; ER_target_S.
InterPro; IPRO1379; Ser_estrs.
Pfam; PF00135; Coesterase; 1.
PROSTIE; PS00102; CARBOXYLESTERASE_B_1; 1.
PROSTIE; PS00122; CARBOXYLESTERASE_B_2; 1.
Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum; Signal; Multigene family.
                                                                          064573; 062679; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Liver carboxylesterase 4 precursor (BC 3.1.1.1) (Carbox Microsomal palmitoyl-CoA hydrolase) (Kidney microsomal carboxylesterase).
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Sprague-Dawley, TISSUB-Liver,
MEDLINE-96190723; PubMed-8611161;
Robbi M., van Schaftlingen E., Beaufay H.;
"Cloning and sequencing of rat liver carboxylesterase if microsomal palmitcyl-CoA hydrolase).";
Biochem. J. 313:821-826(1996).
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EMBL; U10697; AAA64638.1; -.
PIR; S62788; S62788.
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SEQUENCE FROM N.A.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                         13;
                                                                                        DB 1; Length 561;
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I -> F (IN REF. 2).
G -> A (IN REF. 2).
D -> T (IN REF. 2).
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01-UU-1939 (Rel. 11, Created)
01-NOV-1937 (Rel. 35, Last sequence update)
28-REB-2003 (Rel. 41, Last annotation update)
Liver carboxylesterase i precursor (EC 3.1.1.1)
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18 Similarity 41.7%; Pred. No. 1.3e-86;
234; Conservative 123; Mismatches 191;
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STRAIN-Sprague-Dawley, TISSUE-Liver;
MEDLINE-89174514; PubMed=3235453;
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                                                                                                                                                                                                                                    SEQUENCE OF 10-549 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=89050119; PubMed=2973315;
Long R.M., Satoh H., Martin B.M., Kimura S., Gonzalez F.J., Pohl L.R.;
Long R.M., Satoh H., Martin B.M., Kimura S., Gonzalez F.J., Pohl L.R.;
Fat liver carboxylesterase: cDNA cloning, sequencing, and evidence
for a multigene family.";
Biochem. Biophys. Res. Commun. 156:866-873(1988).
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PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum; Signal; Multigene family.
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Pred. No. 8.9e-85;
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S., Go M., Omura T.; sequence of cDNA of
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STRAIN=Sprague Davley; TSSUE=Liver;
MEDLINE=9427470; PubMed=8066016;
Alexson S.E.H., Finlay T.H., Hellman U., Svensson
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InterPro, IPR000379; Ser estrs.
Pfam; PF00135; COesterase; 1.
     Takagi Y., Morohashi K., Kawabata S
Modlecular cloning and mucleotide s
carboxyesterase El of rat liver.",
J. Biochem. 104:801-806(1988).
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EMBL; D30620; BAA06310.1; -.
EMBL; D00362; BAA20565.1; -.
EMBL; X78489; CAA55241.1; -.
PIR; A31284; A31584.
HSSP; P21836; 1MAH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carboxylesterase multigene family.";
Genomics 9:344-354(1991).
-!- FUNCTION: Involved in the detoxification of xenobiotics and in activation of ester and amide prodrugs.
-!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)0 = an alcohol + a
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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MEDLINE=91169540; PubMed=1840565;
Ovnic M., Tepperman K., Medda S., Elliott R.W., Stephenson I Grant S.G., Ganschow N.E.;
"Characterization of a murine cDNA encoding a member of the
 Indels
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01-WAR-1992 (Rel. 21, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Liver carboxylesterase precursor (EC 3.1.1.1) (PES-N)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYML outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A39060; A39060.

HSSP; PAP967; LOE3.

MGD; MGI:9540. E81.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR00379; Ser estrs.

Pfam; PF00135; Coesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.

Glycoprotein; Hydrolase; Serine esTerase; Endoplasmic reticulum; Signal; Multigne family.

SIGNAL
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Pred. No. 3.5e-83;
3; Mismatches 190; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.

LIVER CARBOXYLESTERASE.
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                 RKETITKMIMSTRILLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDAIFVYAIL 454
                                                                                                                                         BIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLP-YIMKFPLNRQAM 394
                                                                                                                                                                                                                                            514 LSLQMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLQLDFTTRVGMKLKEKKMAFWMSLY
                                                                                                                                                                                                                                                                                                                                                                                          455 QTAHYHRDAGLPVYLYEFEHH-ARGIIVKPRIDGADHGDEMYFLFGGPFATGLSMGKEKA
                                                                                                                                                                   DOMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALF
                                                                      RLFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQRDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              novel putative carboxylesterase.";
Biochim. Biophys. Acta 1207:138-142(1994).
-!- FUNCTION: Involved in the detoxication of xenobiotics and in the activation of seter and amide prodrugs.
-!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Syrian golden, TISSUE=Liver;
MEDLINE=94318665; PubMed=8043605;
Sone I., Isobe M., Takabatake E., Wang C.Y.;
"Cloning and sequence analysis of a hamster liver cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carboxylic anion. SUBCELLULAR LOCATION: Microsomal membrane, lumen
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HSSP; P37967; 1QE3.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR00379; Ser_estrs.
Pfam; PF00135; COGETERAGE, 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D28566; BAA05913.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- OSORPEK 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        525 AKEAARPRE 533
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MESAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   esterase from liver microsomal membranes.";
J. Biol. Chem. 262:15316-15321(1987).
-!- FUNCTION: Involved in the detoxification of xenobiotics and in the activation of ester and amide prodrugs.
-!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ::: |:||| | : | |::::::|
WSHVKNITSYPPMCSSDAVSGHMLSELFINRKENIP-LKFSEDCLYLNIYIPADLIKRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 WKGIRDATTYPPGCLQE--SWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTKRPQVVTKYGTLQGKQMHVGK-----TPIQVFLGVPFSRPPLGILRFAPPEPPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carboxylic anion.
-!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.

BY SIMILARITY.

PREVENT SECRETION FROM ER (POTENTIAL).

N-LINKED (GLCNAC. ..).

N-LINKED (GLCNAC. ..).
                                                                                                                                                                         01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Liver carboxylesterase 1 (EC 3.1.1.1).
0ryctoolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordeta; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00102; CARBOXYLESTERASE_B_1; 1.
PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum.
ACT_EITE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation and characterization of a 60-kilodalton glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1133; DB 1; Length 539;
Pred. No. 1.6e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ilarity 41.3%; Pred. No. 1.6e-82;
Conservative 115; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                            "Complete covalent structure of 60-kDa esterase isolated 2,3,7,8-tetrachlorodibenzo-p-dioxin-induced rabbit liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9BC72BC36A49B0BD CRC64;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND ACTIVE SITES SER-195 AND HIS-441.
MEDLINE=88139431; PubMed=3343253;
Korza G., Ozols J.;
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                                                                                                                                     539
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 263:3486-3495(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-70 AND 532-539.
MEDLINE=88033124; PubMed=3667634;
                                 MKLKEKKMAFWMSLYQSQRPE
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258
539
61
363
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363
539 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9986;
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                                                                                                                                         RABIT
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DISULFID
DISULFID
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           559
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::| |: || || : || || || 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 TALFRIFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQ 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPYIMKFPLNR 391
                                            92 PEPPEPWKGIRDATTYPPGCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 PLPPQPWEGVRDASINPPMCLQDV-ERMSNSRFTLNEKWKIFPISEDCLTLNIYSPTEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 AGDKRPVMYWIHGGSLRVGSSTSHDGSALAAXGDVVVVTVQYRLGIFGFLSTGDKHMPGN
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                                                                                                                                                                                                                                                                              reticulum.
-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.

LIVER CARBOXYLESTERASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
PREVENT SECRETION FROM ER (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIRS. S34607; S34607; HSSP; P344607; PIRS. S34607; S34607; LQB3.

HSSP; P37967; LQB3.

HSSP; P37967; LQB3.

HGD; MGD; MGD; MGG1102773; ES31.

InterPro; IPR002019; Ser_estrs.

PFam; PF00135; Coesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 1; 1.

PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

PROSITE: PS00122; CARBOXYLESTERASE B 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
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                                                                                                                                                                                                                                       carboxylic anion.
-!- SUBCELLULAR LOCATION: Microsomal membrane,
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61509 MW;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 MYFLFGGPFATGLSMG---KEKALSLQMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLQ 55,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        521
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                                                                                                                                                                                                                                                                                                                                                                                                                    68 VGPLRFAPPEPPEPPEWSGVRDGTSEPAMCLQTDFMRPQI-----SKERKIILPTISMSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 RVSNKOMRFLQLNFQRDPBEIIWSMSP-VVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 CGWGVPLFWGLDHVIKNITRETLPAFLKSRAEHMMLPPECSDLLMQEYMGDV--EDPQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 RNRMMDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHHARGI---IVKPRTDGADHGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 CWSLTLCLMAQTALGALH---TKRPQVVTKYGTLQGKQMHV--GKTPIQVFLGVPFSRPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGILRFAPPEPPEPWKGIRDATTYPPGCLQESW--GQLASMYVSTRER---YKWLRFSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLYLNVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 FNWLLPYIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKML
                                                                                                                     LIVER CARBOXYLESTERASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
[1]
                                                                 Endoplasmic reticulum,
                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                                                                                                                                                                                                                                          ); DB 1; Length 561;
1.1e-76;
                                                                                                                                                                                                                                                                                                              34.1%; Score 1060; DB 1; Length 5 41.1%; Pred. No. 1.1e-76; ive 97; Mismatches 191; Indels
                                                                                                                                                                                                                                                                              48EA11E422475321 CRC64;
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10-NOV-1997 (Rel. 35, Last sequence update)
20-FEB-2003 (Rel. 41, Last annotation update)
Liver carboxylesterase precursor (EC 3.1.1.1)
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Glycoprotein; CARBOXYLESTERASE B 2; 1. Glycoprotein; Hydrolase; Serine esterase; is Signal; Multigene family.
SIGNAL
CHAIN
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01-NOV-1997 (
28-FEB-2003 (
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ESTM MOUSE
AC 063880;
DT 01-NOV-1997
DT 28-FEB-2003
DE inver carbox
GN ESJ1.
CS Mus musculus
CC Eukaryota; M
CC Mammalia; EU
CO NGBI_TAXID=1
RN [1]
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1 AND 2), SEQUENCE OF N-TERMINUS, TISSUE WITH NEUREXIN 1-BETA; NEUREXIN 2-BETA AND
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MEDLINE=2126491; PubMed=11329178;

Gilbert M., Smith J., Roskams A.J., Auld V.J.;

Gilbert M., Neuronal cell surface protein thought to be involved in - FMNGTION; Neuronal by forming intercellular junctions through binding to beta-neurexins. Seems to play role in formation or maintenance of synaptic junctions. In vitro, triggers the de novo maintenance of synaptic structures (By similarity).

Formation of presynaptic structures (By similarity).
                                                                          LQ----NLAIM----DQDVLLLHFTPPSIPMSEDCLYLNIXSPAHAREGSDLPVMVWIHG
                                                                                                                                      285 KVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKWRFLQLNFQRDPEEIIWSMSPV
                                                                                                                                                                                              345 VDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLPYIM-----KFPLNRQAMRK--E
                                                                                                                                                                                                                                                                                                                                                         HYHRDAGLPVYLYEFEH------HARGIIVKPRTDGADHGDEMYFLFGGP-FATG
                                                                                                                                                                                                                                                                                                                                                                                                                     506 LSM-GKEKALSLOMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLQLDFTTRVGMKLKEK
SEDCLYLNVYAPARAPGDPQLPVMVWFPG
                                                                                                                   QENIAARGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPL
                                                                                                                                                                                                                                                                                               398 TITKMLWSTRTLINITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDATFVYATLQTA
                                                                                                                                                                                                                                                                                                                                                                                       398 HLQR-SHAPTYFYEFQHRPSFTKDLRPPHVR-----ADHGDEVVFVFRSHLFGSK
                                                           GAFIVGAASSYEGSDLAAREKWLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWV
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 271:2676-2682(1996)
 LOESWGOLASMYVSTRERYKWLRF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Forebrain;
MEDLINE=96162010; PubMed=8576240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Rattus norvegicus (Rat)
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RLOFW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation, properties, and the complete amino acid sequence of a second form of 60-kba glycoprotein esterase. Orientation of the 60-kba proteins in the microsomal membrane.";
J. Biol. Chem. 264:12533-12545(1898).-!- FUNCTION: Involved in the detoxification of xenobiotics and in the
                 QAMRKETITKMLWSTRTLL---NITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDAT
                                    DKWEHLSQEDLLENSRPLLAHMQLPPEIMPTVIDEYLDNGS--DESATRYALQELLGDIT
                                                                                             101 LVIPTLIFSKYLQDAGCPVFLYEFQHTPSSFAKFKPAWVKADHSSENAFVFGGPFLTDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 THTGQVRGSLVHVEGTDAGVHTFLGIPFAKPPLGPLRFAPPEPAEAWSGVRDGTSLPAMC
                                                                             FVYATLQTAHYHRDAGLPVYLYEFEHHARGII-VKPRTDGADHGDEMYFLFGGPFATGLS
                                                                                                                                      -----MGKEKALSLOMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLOLDFTTRVGM
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PREVENT SECRETION FROM ER (POTENTIAL)

N-LINKED (GLCNAC. . .).

CS7DDD76A13A9C52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Buteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A34329; A34329.
HSSP; P37967; LOE3.
HSSP; P37967; LOE3.
HINTERPRO; IPRO003018; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PRO01125; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activation of ester and amide prodrugs. CATALYTIC ACTIVITY: A carboxylic ester + H(2)0 = an alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 993; DB 1; Length 532;
Pred. No. 2.3e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                      P14943;
01-APR-1990 (Rel. 14, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                   532 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the type-B
                                                                                                                                                                                                KLKEKKMAFWMSLYQSQRPEKQRQ 583
                                                                                                                                                                                                                           KLKKGRLOFWTETLPRKIOEWHRE 544
                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89308686; PubMed=2745458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85;
                                                                                                                                                                                                                                                                                                                                                                              Liver carboxylesterase 2 (EC 3 Oryctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59058 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.9%;
larity 41.5%;
Conservative 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid
                                                                                                                                                                                                                                                                                                     STANDARD;
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253
529
249
532 AA;
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226; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrrolidone or MOD RES
ACT_SITE 2
ACT_SITE 4
DISULFID 2
                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus
                                                                                                                                                                                                                                                                                                     RABIT
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Best Local S
Matches 226
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 ----PVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNW 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 ILGPVVQFLGVPYATPPLGARRFQPPEAPASWPGVRNATTLPPACPQNLHGALPAIMLPV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ASMYVSTRERYKWLRFSEDCLYLNVYAPAR------APGDPQL-- 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 WFTDNLEAAATÝVQNQ-----SEDČLÝLNLÝVPTEDGPLTKKRDEATLNPPDTDIRD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALFRLFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQR 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 WSLTLCLM----AQ------TALGALHTKR-PQVVTKYGTLQGKQMHVGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 WILLALCLVGLAGAORGGGPGGGAPGGPGLGLGSLGEERFPVVNTAYGRVRGVRRELNNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 ---piQVFLGVPFSRPPLGILRFAPPEPPEPWKGIRDATTYPPGCLQESWGQL-----
                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.3%; Score 849; DB 1; Length 836;
ilarity 33.2%; Pred. No. 1.3e-59;
Conservative 92; Mismatches 191; Indels 150; Gaps
4/Beta 4B5B. Interacts with neurexin 2-beta isoforms 3/Beta 4B5A
            4/Beta 4B5B, 7/Beta 4B5A6 and 8/Beta 4B5B6. Interacts with neurexin 3-beta. Probably interacts through its C-terminus with DLG4/PSD-95 third PDZ domain (By similarity). SUBCELLULAR LOCATION: Type I membrane protein (Potential). ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                 IsoId=062888-2; Sequence=VSP 007533;
-!- TISSUE SPECIFICITY: Expressed in brain, spinal chord and dorsal root ganglion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROBABLE.
NEUROLIGIN 2.
EXTRACELLUIAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
Missing (in isoform 2).
/FIIG-VSP_007533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1AD51CBIBE4BF9CF CRC64;
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InterPro; IPR000460; Neuroligin.
InterPro; IPR000319; Ser_estrs.
PERM; PR00135; Coesterase; 1.
PRINTS; PR00195; NEUROLIGIN.
PRINTS; PR00190; NEUROLIGIN.
PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
PR061126; PS01019; CARBOXYLESTERASE_B_2; 1.
                                                                                                                                   IsoId=Q62888-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            836 AA; 90961 MW;
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HSSP; P37967; 1QE3.
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ses 215; Conserv
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q	: 294 AIS	: :: :: :: ::
δ	333 DPE	DPEELIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLE376
qq	343 QPA	OPARYHIAFGPVVDGDVVPDDPEILMQQGEFLNYDMLIGVNQGGGLKFVEDSAESEDGVS 402
δ	377	FNWLLPYIMKEPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVN 429
qq	403 ASA	403 ASAFDFTVSNFVDNLYGYPEGKDVLR-ETIKFMYTDWAD 440
ò	430 EHD	EHDWKMIRNRMMDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHHARGIIVKPRTDG 487
QQ	441 RDN	RDNGEMRRKTILALFTDHQWVAPAVATAKTHADYQSPVYFYTFYHHCQAEGRPEWAD 497
ò	488 ADH	ADHGDEMYFLFGGPFATGLSMGK-EKALSLQMMKYWANFARTGNPNDGNLP 537
ДĢ	498 AAH	AHGDBLPYVFGVPMVGATDLFPCNFSKNDVMLSAVVMTYWTNFAKTGDPNQ-PVPQDTK 556
δy	538	CWPRYN-KDEKYLQLDFTTRVGMKLKEKKMAFWMSL 572
qq	557 FIH	FIHTKPNRFEEUVWSKFNSKENGYLHIGLKPRVRDNYRANKVAFWLEL 604

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 MRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPFSRPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ol-JUN-2002 (TrEMBLrel. 21, Created)
Ol-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Ol-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Ol-OCT-2003 (TrEMBLrel. 25, Last annotation update)
BC026374.
BC026374.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae, Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 70.1%; Score 2182.5; DB 11; Length 556; Best Local Similarity 71.8%; Pred. No. 5.5e-177; Matches 400; Conservative 68; Mismatches 86; Indels 3;
Q86uk2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    556 AA.
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                           Q9ULX1
Q8VCC2
Q81034
Q91034
O91034
O924V3
Q82533
Q924V3
Q81074
Q81074
Q81089
Q8
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Q95n05 canis famil
Q46421 macaca fasc
Q96ee8 homo sapien
Q81429 homo sapien
Q77540 oryctolagus
Q91135 rattus norv
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                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                       MAALRWVQENI AAFGGDPGNVTLFGQSAGAMSISCLWMSPLASGLFHRAISQSGTALFRP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
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Miyazaki M., Sai H., Taira H., Yamashita T.;
Miyazaki M., Sai H., Taira H., Yamashita T.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB094147; BAC75712.1; -.
GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR000379; Ser estreseB.
InterPro; IPR000379; Ser estre.
PFam; PF00135; COesterase; 1.
PROSITE; PS00122; CARROXVIESTERASE B.1; 1.
PROSITE; PS00141; CARBOXVIESTERASE B.2; 1.
SEQUENCE 566 AA; 62231 MM; 4677D3F67205AD53 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Li
01-OCT-2003 (TrEMBLrel. 25, Li
Carboxylesterase.
          Conservative
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Takahashi Baconas To the EMBL/Genbank/DDBJ databases.

L- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

EMBL; AK094783; BAC04422.1; ENGOSOLS, ENGOSOLS, ENGOSOLS, ENGOSOLS, ENGOSOLS, CarbesteraseB.

InterPro; IPR002018; CarbesteraseB.

EMBL; PR00155; CosteraseB.; L.

Familarian Control of CosteraseB.
                                                                                                             VYAPVLAPGAPLLPVMVWFPGGAFLAGSASTYEGSELAARGKVVLVFLOYRLGILGFFST
                                                                                                                                                                                                                  GNSHARGNWGLLDQIAALRWVQENIEAFGGDPDSVTLFGQSAGAMSVSGLMVSPLAQGLF
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HRAISQSGTALFRLFITSNPLKVAKKVAHLAGCNHNSTQ1LVNCLRALSGTKVMRVSNKM
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                                                                                  VYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLST
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ37464.

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 9.3e-156;
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Hypothetical protein; Hydrolase.
SEQUENCE 367 AA; 41851 MW; 95671668E6F
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Best Local Similarity
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FHRAISOSGTALFRLFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNK 322
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                                                                  TGDEHGRGNWGHLDQLAALRWVQENIANFGGNPGSVTIFGESAGGESVSVLVLSPLAKNL
LGPLRFAPPQAAEPWNFVKNTTSYPPMCSQDAVGGQVLSELFTNRKDNIPLKFSEDCLYL
                                          NVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLS
                                                                                                                                 TDDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGL
                                                                                                                                                                                                                                                                                                                                                                                                383 YIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Carboxylesterase precursor (EC 3.1.1.1).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Elwaryota, Metasca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sone T., Takabatake E., Isobe M.;

Sone T., Takabatake E., Isobe M.;

"cDNA cloning and characterization of a monkey liver
T carboxylasterase.";

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
C -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMI
R EMBL; AB010633; BAA24523.1; -.
R HSSP; P21936; IMAH.
R GO; GO:0016789; F:Berine esterase activity; IEA.
R GO; GO:0016789; F:Serine esterase activity; IEA.
R InterPro; IPRO00210; CarbesseraseB.
R InterPro; IPRO00210; CarbesseraseB.
R PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
R PROSITE; PS0012; CARBOXYLESTERASE_B2; 1.
R HYDGolase; Signal.
T SIGNAL
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566 CARBOXYLESTERASE.
62510 MW; 808040F1A4077297 CRC64;
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41.2%; Score 1282; DB 6;
Best Local Similarity 45.3%; Pred. No. 2.8e-100;
Matches 251; Conservative 116; Mismatches 177;
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                                                                                                                                                                                                                        KWRFLØLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLL 381
                                                                                                                                                                                                                                                                                                                                       PFATGLSMGKEKALSLOMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLQLDFTTRVGMK 560
INIYTPVDLRKKNRLPVMVWIHGGGLMVGGASTYSGLVLSAHENVVVVTIQYRLGIWGYF 179
                                                                                                                                 LFHRAISQSGTALFRLFITSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSN 321
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                                                                  SEQUENCE FROM N.A.
MEDIINE=21237951; PubMed=11339814;
HOSOKawa M., Suzuki K., Takahashi D., Mori M., Satch T., Chiba K.;
HOSOKawa M., Suzuki K., Takahashi D., Mori M., Satch T., Chiba K.;
"Purification, Molecular Cloning, and Functional Expression of Dog
Liver Microsomal acyl-CoA Hydrolase: A Member of the Carboxylesterase
Mulligene Family."
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                                                                                                                                                                                                                                                                                                             PYIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMM
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                                                                                                                                                                                                                                                  Arch. Biochem. Biophys. 389:245-253(2001).
-!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
EMBL. AB023629; BAB60696.1; -.
GO; GO: 0016787; F: Hydrolase activity; IEA.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR00379; Ser estrs.
Pfam, PF00135; COGSterase; 1.
PROSITE; PS00121; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
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Canis.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae,
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Last annotation update)
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41.3%; Score 1284; DB 6;
Best Local Similarity 45.3%; Pred. No. 1.9e-100;
Matches 253; Conservative 106; Mismatches 192;
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ELFTURKENIPLKLSEDCLYLNIYTPADLTKKNRLPVMVWIHGGGLMVGAASTYDGLALA 158
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                                                       63 QMHVGKTPIQVFLGVPFSRPPLGILRFAPPEPPEPWKGIRDATTYPPGCLQE-SWGQLAS 121
                                                                                                                                                                                                                               GOSAGAMSISGLMMSPLASGLFHRAISOSGTALFRLFITSNPLK-VAKKVAHLAGCNHNS 300
                                                                                                                                                                                                                                                                                                          SAVWVHCLRQKTEEELLETTLKMKFLSLDLQGDPRESQPLLGTVIDGMLLLKTPEELQAE
                           -----HPSSPPVVDTVHGKVLGKFV
                                                                                                                                                                                                                                                                                      301 TQILVNCLRALSGTKVMRVSNKMRFLQLNFQRDPEBIIWSMSPVVDGVVIPDDPLVLLTQ
                                                                                                                                                                                      SIEGFAQPVAIFLGIPPAKPPLGFLRFTPPQPAEPWSFVKNAISYPPMCTQDPKAGQLLS
                                                                                                               122 MYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLA
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                                                                                                                                                                                                                                                                                                                                             GKVSSVPYLLGVNNLEFNWLLPYIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 IVKPRTDGADHGDEMYFLFGGPFATGLSMGKEKALSLQMMKYWANFARTGNPNDGNLPCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
EMBL, AB025027; BABSE566.1; --
GO, GO:0016797; F:lydrolase activity; IEA.
InterPro; IPR002018; CarbesteraseB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. TISSUB-Brain; Hosokawa M., Momori C., Tsukada E., Chiba K.; "CDNA cloning and expression of carboxylesterase isizymes from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mori M., Hosokawa M., Tsukada E., Ogasawara Y., Chiba K.; "CDNA cloning and stable expression of human brain carboxylesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NOSI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRYNKDEKYLQLDFTTRVGMKLKEKKMAFWMSLYQSQRPEKQRQ 583
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Last annotation update)
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                3 LPALVLATL--AASAAWG----
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
Brain carboxylesterase hBr2.
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                                                        EPPEPWKGIRDATTYPPGCLQES-WGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAP 151
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                           89
               TALFRLFITSNPLK-VAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNF
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                                                                                                                                                                                                                                                            VALTAVLVKKGDVKPLAEQIAIAAGCQTTTSAVMVHCLRQKTEEELLETTLKMKFFSLDL
                                                                                                                                                                                                                                                                                                                                                391 ROAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDATFV
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 LMAQTALGALHTKRPQVV-TXYGTLQGKQMHV-GKT-PIQVFLGVPFSRPPLGILRFAPP
                                                                                                                 GDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUBLELLULY R.;
Strausberg R.;
Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
-: SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
GD, GO:0016787; F: Hydrolass activity; IEA.
InterPro: IPR002018; CarbesteraseB.
InterPro: IPR00379; Ser_estrs.
Fam: PRO0115; COOSterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
PROSITE; PS00121; CARBOXYLESTERASE_B_2; 1.
Hypothetical protein; Hydrolase.
SEQUENCE S66 AA; 62269 MW; 3B86CBAIC42BAA0F CRC64;
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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40.6%; Score 1265; DB 4; Length 5
Best Local Similarity 43.2%; Pred. No. 7.9e-99;
Matches 252; Conservative 111; Mismatches 189; Indels
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Last annotation update)
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TTLFAKKAVEKPQ
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MLGYPLSEGKLDQKTATELLMKSYPIVNVSKELTPVATEKYLGGTDDPVKK--XDLFLDM
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
carboxylesterase (EC 3.1.1.1) (Fragment).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
    THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY
                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                Length 565;
                                                                                                                                                                                                                                                                              tch
al Similarity 43.8%; Score 1260; DB 6; Length 5
al Similarity 43.8%; Pred. No. 2.1e-98;
245; Conservative 119; Mismatches 180; Indels
                                                                                                                                                                                                                                     565 AA; 62291 MW; 0ACD61400CC81D2F CRC64;
-!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLIS EMBL; AF036590, AAC3258.1; -- PD3.1K4Y; 0.1-MAY-0.2 GO; GO:0016787; F:hydrolase activity; IEA. GO; GO:0004759; F:scrine esterase activity; IEXINTERPRO: PR0022018; CarbesteraseB. LinterPro: IPR002379; Ser_estrs. Pfam; PF00135; COSECERASE; I. PR0031FEARSE B.; 1. PR0SITE; PS00121; CARBOXYLESTERASE B.; 1. PROSITE; PS001941; CARBOXYLESTERASE_B_2; 1.
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SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
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                                                                                                                                                                                                                                          83
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                                                                                                                                                                                                                                                                                                                              LGILRFAPPEPPEPWKGIRDATTYPPGCLQES-WGQLASMYVSTRERYKWLRFSEDCLYL
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                                                                                                                                                                                                                                          WILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMHVG--KTPIQVFLGVPFSRPP
                                                                                                                                                                                                                                                                                                                                                                                                                NVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383 YIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD
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                                                                                                                                                                                                                                                                                   WL--PDLVLTSLATSMAWGYPSLPPVVDTVQGKVLGKYVSLEGFAQPVAVFLGVPFAKPP
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Potter P.M., Pawlik C.A., Morton C.L., Naeve C.W., Danks M.K.;
Isolation and partial characterization of a cDNA encoding a rabbit liver carboxylesterase that activates the prodrug irinotecan (CPT-11).";
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                                                                                                                                                          565;
                                                                                                                                                                                              Indels
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                                                                                                               565 AA; 61962 MW; E255244C2CAA9A1E CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Liver carboxylesterase (EC 3.11.1).
Chyctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Lagomorpha; Leporidae; Oryctola
                                                                                                                                                      40.6%; Score 1264; DB 4;
44.7%; Pred. No. 9.6e-99;
tive 106; Mismatches 195;
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      InterPro; IPR000379; Ser_estrs.
Pfam; PF000135; Coesteraes; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
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Cancer Res. 58:2646-2651(1998)
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hes 250;
                                                                                          Hydrolase.
SEQUENCE
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Metazoa;
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      28 LCWSLTLCLMAQTALG-----ALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPFSR 81
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40.3%; Score 1254; DB 11;
Best Local Similarity 42.8%; Pred. No. 6.8e-98;
Matches 240; Conservative 120; Mismatches 183;
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RLKDKEVAFWSELRAKEAAEE
                                                                                                                      62130 MW;
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01-DEC-2001 (TEMBLrel. 19, Ca
01-DEC-2001 (TEMBLrel. 19, Le
01-OCT-2003 (TEMBLrel. 25, Le
Carboxylic ester hydrolase (ER
Rattus norvegicus (Rat).
Lee W., Jung C.Y.;
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NON TER
SEQUENCE
Ryu J.W.,
"Rattus no
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                                                                                                                                                                     Wallace T.J., Kodsi E.M., Langston T.B., Gergis M.R., Grogan W.M.;
"Mutation of Residues 423 (Met/Tile), 44 (Thr/Met), and 506 (Asn/Ger)
Confer Cholesteryl Esterase Activity on Rat Lung Carboxylesterase.
SER-506 IS REQUIRED FOR ACTIVATION BY CAMP-DEPENDENT PROTEIN KINASE.";
J. Biol. Chem. 276:3115-33174 (2001).
-! SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
EMBL, L81144; AAL00849:1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLGSLRFAPPQPAEPWNFVXXVTTSYPPMCSQDAVGGQVLSELFTNRKENIPLQFSEDCL
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Sciurognathi, Muridae, Murinae, Rattus.
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GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0004759; F:serine esterase activity; IEA.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR00379; Ser_estrs.
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PROSITE; PS00122; CARBOXYLESTERASE B 1;
PROSITE; PS00941; CARBOXYLESTERASE B 2;
                                                                                                                         STRAIN=Sprague-Dawley, TISSUE=Lung;
MEDLINE=21413896, PubMed=11429416;
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Chordata; S
Rodentia; S
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PRELIMINARY:

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Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                92
                                                                                                                                                                                                                                                                                                                                                  89
                                                                                                        TISSUE-Liver;
Islam M.R., Waheed A., Shah G.N., Tomatsu S., Sly W.S.;
Imman Bgasyn Binds beta-Glucuxonidase But Neither the Esterase Active Site of Egasyn Nor the C Terminus of beta-Glucuxonidase Is Involved in Their Interaction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TALFRLFITSNPLK-VAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QRDPEELIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWLLP-YIMKFPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 NRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEGOLDQXTAMSLLWKSYPLVCIAKELIPEATEXYLGGTD--DTVKKKDLFLDLIADVMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYATLQTAHYHRDAGLPVYLYBFEHH-ARGIIVKPRTDGADHGDEMYFLFGGPFATGLSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKEKALSLOMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLQLDFTTRVGMKLKEKKMAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 LMAQTALGALHTKRPQVV-TKYGTLQGK--QMHVGKTPIQVFLGVPFSRPPLGILRFAPP
                                                                                                                                                                                                                                                                                                                                                                                                               152 GDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSG
                                                                                                                                                                    FAMILY.
                                                                                                                                                                                                                                                                                                             Gaps
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                         567;
                                                                                                                                                        Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE
EMBL; AF177775; AAD53175.1; -.
                                                                                                                                                                                                                                                                                         DB 4; Length
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                     567 AA; 62448 MW; CC445067DC79EC59 CRC64;
                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                             187;
                                                                                                                                                                                                                                                                                      40.1%; Score 1248.5; Di
Local Similarity 44.7%; Pred. No. 2e-97;
hes 248; Conservative 109; Mismatches 18
                                                                                                                                                                                      HSSP; P21836; 1MAH.

G0; G0:0016787; F:Nydrolase activity; IEA.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR00379; Ser_estrs.

Pfam; PF00135; Coesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
          Created)
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WTNLFAKKAVEKPPQ
        01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                 (Human)
                                                                                                 SEQUENCE FROM N.A.
                                                                              NCBI_TaxID=9606;
                                       Egasyn.
Homo sapiens
                                                                                                                                                                                                                                                               Hydrolase.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 IIPMIMGYPLSEGKLDQKTANSLLWQSYPTVKIPKNLIPWATEKYLGGTDDPAKK--KDL 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MMDIVQDATEVYATLQTAHYHRDAGLPVYLYEFEHHARGII-VKPRTDGADHGDEMYFLF 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLPYIMKFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 RPPLGILRFAPPEPPEPWKGIRDATTYPPGCLQES-WGQLASMYVSTRERYKWLRFSEDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYLNVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNKWRFLQLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 WI--LCWSLTLCLMAQTALGALHTKRPQVV-TKYGTLQGKQMHVG--KTPIQVFLGVPFS
                                                                                                                                                                                                                                                                                                                                                                                                                          arylhydroxamic acids.";

Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.

SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

BENBL; D50578; BAA2364.1;

HSSP; P21836; IMAH.

GO; GO:0016787; F:hydrolase activity; IEA.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR00319; Sar estrs.

PFAM; PF00135; COesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE_B.1; 1.

PROSITE; PS00121; CARBOXYLESTERASE_B.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                           Mesocricetus auratus (Golden hamster).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Syrian golden; TISSUE=Liver;
SONE T., Ishida Y., Takabatake E., Wang C., Isobe M.;
Cloning and expression of a hamster liver cDNA encoding a novel
"Cloning and expression of a hamster liver cDNA encoding a novel
carboxylesterase which catalyzes the activation of carcinogenic
                                                                                                                                                                                                                                                                                                                                                                                  novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOXYLESTERASE.
8273233A59DF1ED0 CRC64;
               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Carboxylesterase precursor (BC 3.1.1.1).
Mencall Carboxylesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1247; DB 11;
Pred. No. 2.7e-97;
9; Mismatches 189;
  Ą
  265
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PRT;
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Best Local Similarity 42.7%; Pre
Matches 240; Conservative 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565 AA; 62188 MW;
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
565
                                                                                                                                                                                                                                             Mesocricetus.
NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Signal
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STRAINS-CS7EL/61; TISSUE=Colon;

MEDLINE=22354683; PubMed=12466851;

The FANTOM Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

Thailysis of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs.";

I Mally sis of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs.";

I Nature 420:563-573(2002).

C -1 SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

REMBL; ARO78879; BAC37439-1;

R MGD; MGI: 2148202; Cee3.

R GO; GO:0016787; F: hydrolase activity; IEA.

R InterPro; IPR002018; CarbesteraseB.

R InterPro; DFR002018; CarbesteraseB.

R InterPro; DFR002018; CarbesteraseB.
140
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                                                                                                        500 GPFAIGLSMGKEKALSLOMMKYWANFARIGNPNDGNLPCWPRYNKDEKYLQLDFTTRVGM
                                                                                                                                                                                                      476 SPFLKDGASEBETNLSKOWVMKFWANFARNGNPNGGGLPHWPEYDQKEGYLKIGASTQAAQ
                                                                         441 MDIVQDATFVYATLQTAHYHRDAGLPVYLYEFEHHARGI-IVKPRTDGADHGDEMYFLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 LCWSLTLCLMAQTALG-----ALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPFSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLGILRFAPPEPPEPWKGIRDATTYPPGCLQES-WGQLASMYVSTRERYKWLRFSEDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 PPLGSLRFAPPOPAEPWSFVKKYTTSYPPMCSODAVGGOVLSELFTNRKENIPLOFSEDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLNVYAPARAPGDPQLPVMVWPPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 43.2%; Fred. NO. 3.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             565 AA; 61787 MW; E85A9976F9916B34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.0%; Score 1244.5; DB
43.2%; Pred. No. 4.4e-97
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PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
                                                                                                                                                                                                                                                                          578
                                                                                                                                                                                                                                                                                                                      536 RLKDKEVSFWAELRAKESAQRP 557
                                                                                                                                                                                                                                                                       560 KLKEKKMAFWMSL---YOSQRP
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20,
25,
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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01-MAR-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Carboxylesterase 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=10090;
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SEQUENCE
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Best Local S:
Matches 243
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MEDLINE2=2186045; PubMed=11470237;

Dolinsky V.W. Sipione S., Lehner R., Vance D.E.;

Dolinsky V.W. Sipione S., Lehner R., Vance D.E.;

The cloning and expression of a murine triacylglycerol hydrolase cDNA and the structure of the corresponding gene.";

Biochim. Biophys. Acta 1532.162-172 (2001).

--- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASZ/LIPASE PAMILY.

EMBL; AR78771; AR58067.1;

--- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASZ/LIPASE PAMILY.

MOD; MOI12148202; Ces3.

GO; GO:0016787; F:hydrolase activity; IEA.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR002018; CarbesteraseB.
                       GGPFATGLSMGKEKALSLOMMKYWANFARTGNPNDGNLPCWPRYNKDEKYLOLDFTTRVG
                                                    178 FSTGDEHSRGNWGHLDQVAALRWVQDNIANFGGNFGSVTFFGESAGGFSVSVLVLSPLAK
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
                                                                                                                                                                                                                                                                                            565
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01-CCT-2003 (TrEMBLrel. 25, Last annotat
Triacylglycerol hydrolase (EC 3.1.1.1).
CES3.
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535 HRLKDKEVIFWTELRAKEAAER 556
                                                                                                                  MKLKEKKMAFWMSLYQSQRPEK 580
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321 NKMRFLQLNFQRDPERIIWSMSPVVDGVVIPDDPLVLLTQGKVSSVPYLLGVNNLEFNWL 380
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58 PPLGSLRFAPPQPAEPWSFVKNTTSYPPMCSQDAVGGQVLSELFTNRKENIPLQFSEDCL 117
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                                                      141 YINVYAPARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGF
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time : 45 secs
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1. Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

2. -i. SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY. BR. MGD; MGI:2148202; Ces3.

3. MGD; MGI:2248202; Ces3.

4. GO; GO:0016787; F:hydrolase activity; IEA.

5. GO; GO:004789; F:serine esterase activity; IEA.

5. REPORTS: PRO00379; Ser_estrs.

5. REPORTS: PRO0125; CARBOXYLESTERASE B 1; 1.

5. REPORTS: PRO0125; CARBOXYLESTERASE B 1; 1.
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STRAIN=CS7BL; TISSUB=Liver;
HOSOKawa M., Nakamura T., Nakata F., Takahashi D., Sakae M., Satoh
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Carboxylesterase MH1 (EC 3.1.1.1).
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ALIGNMENTS

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/note="unnamed protein product"
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Pred. No. 0;
); Mismatches
                                 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
m Pharmaceuticals, Inc.
Location/Qualifiers
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Matches 1752; Conservative 0;
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                                                                                             Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Kapeller-Libermann, R. and Silos-Santiago, I.
Methods of using 18903 to treat pain and pain-related disorders
Patent: WO 0244357-A 1 06-UUN-2002;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Sequence 1 from Patent W00244357,
AX469746 GI:21901868
  Query Match
Best Local Similarity
Matches 1752; Conserv
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Contact: MGC help desk
Email: cappbs-remail.inh.gov
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PNGEKLPYWPRFDKDEKYLQLDFDTRVGVKLKEKKMAFWSQLRQSQKP"
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2599,
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                                                                                                                             1106 TGACTGGAAGATGCTACGAAACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTA
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       TATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCA
                                                                         TGACTGGAAGATGCTACGAAACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTA
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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N AY358504.1 GI:37182130 DS FLI CDNA. Homo sapiens (human) NISM Homo sapiens Eukaryotes, Metazoa; Chordata; Craniata; Mammalia; Eutheria; Primates; Catarrhini. NCE 1 (bases 1 to 2456) ORS Clark,H.F., Gurney,A.L., Abaya,E., Baker, Chen,J., Chow,B., Foster,J., Growley,C., Chow,B., Eaton,D., Foster,J., Grimaldi,C., Edelons,S., Hang,A., Kim,H.S., Klimowsk. I che,J., Lewis,L., Liao,D., Mark,M., Robb: Schoenfeld,J., Seshagiri,S., Simmons,L.,	Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, W., Yun, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Goddwski, P. TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment DOURNAL Genome Res. 13 (10), 2265-2270 (2003)	Clark, H.F. Direct Submitted Submitted Inc., 1 DN	/db_xref="taxon:9606" /clone="DNA44179" gene 1.2456 /locus_tag="UNQ440" CDS /locus_tag="UNQ440" /note="PRO873"	/coduct="carboxylesterase Hlo" /product="carboxylesterase Hlo" /product="carboxylesterase Hlo" /protein_id="AAQ88868.1" /db_xref="c1:37182111" /db_xref="c1:37182111" /translation="MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNF GNLGSTSTPATTSAPSGSGTGLFGSKPATCGTTGGTNTGALHTKRPQVVTKYGTLGG KQMHVGKTPIQVFLGVPFSRPPLGILRFAPPEPEPEPWKGIRDATTYPPGWSLALSPGW SAVARGRITATSARVQASLLAOPLSVWGYRCLQSSWGQLAARWYSTRERSKE DCLYLNVYAPARAPGDPQLPVWWFPGGAFLVGAASSYEGSDLAAREKVULVFLGHRL GIFGFLSTDSSHARGMVGLLDQMAALRWVQRNIAARGGDPONVTLFGQSACAMSISGL	MMSPLASGLEHRAISOSGTALFRLFITSNPLKVR SGTKVMRVSNRARFLQLNFQRDÐFEIINSMSPVN LGVNNLLEFNMLLEFNY ITKEOVÞLVVEFLLDNVNR QTAHYHRETPNMGICPAGHATTRMKSTCSWILÞQ		GGTGCCTTGCACACCAGGGCCTCAAGTGGTCACCAAAAAATGGAACCCTGCAAGGAAAAAAGGCCTTGCACCAACGGAAGAAAAGGCCTTGCACCCACC	187 CACATIGCATGATGATGATGATGATGATGATTTTTAGGATGCCCTTCATGAGACCCT 507 448 CAGATGCATGATGATGATGATTTTTTAGGATGCCCTTCAGAGACTCT 507 247 CCTCTAGGTATCCTCAGGTTTGCACCTCCCAGACCCTGGAAAGGAAAGAAA	GATGCTACCACCTACCGCCTG
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AY358504 2456 bp mRNA linear PRI 03-OCT-2003 Homo sapiens clone DNA44179 carboxylesterase Hlo (UNQ440) mRNA, complete cds. AY358504

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712 GTGACCCTGTTCGGCCAGTCGGCCATGAGCATCATCGGCATGATCATCATCACCCCCAGGGT 71 72 73 74 74 74 74 74 74 74	OY 1552 ATGATGAAATACTGGGCCAACTTTGCCCGCACAGGAAACCCCCAATGATGGGAATCTGCCC 1611 Db 1399 ATGATGAAATACTGGGCCAACTTTGCCCGCACCCAATGATGGGGAATCTGCCC 1458 OY 1612 TGCTGGCCACGCTACAACAACTTTGCCCGCACCCCAATGATGGGAATCTGCCC 1458 Oy 1612 TGCTGGCCACGCTACAACAAGAATACTACCTGCAGCTGAATTTACCACAAGAGTG 1671 Db 1459 TGCTGGCCACGCTACAAGAAGAAGAAGAAGAACCTGCAGCTGAATTTTACCACAAGAGTG 1518 Oy 1672 GGCATGAAGCTCAAGGAAAAGAAGAAGAAGAAGAAGAAGAATTTTGGATGAT
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Miyazaki, M., Sai, H., Taira, H. and Yamashita, T.
Miyazaki, M., Sai, H., Taira, H. and Yamashita, T.
Direct Submission
Submitted (19-007-2002) Masco Miyazaki, Iwate University,
Department of Agro-bioscience, Faculty of Agriculture; 3-18-8 |
Morioka, Iwate 020-8550, Japan (E-mail:cdg83700@par.odn.ne.jp,
Tel:81-19-621-6157, Fax:81-19-621-6177)
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                                                                                                                                                                                                                                                                                                          Miyazaki,M., Sai,H., Taira,H. and Yamashita,T.
Molecular cloning of the feline liver carboxylesterase
Unpublished
                                                                                                                                                                                       Felis catus (cat)
Felis catus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .1985

Organism="Felis catus"

Mol_type="mRNA"

/db Aref="taxon:9685"

/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue type="liver"
dev stage="adult"
1. 1985
|gene="CES1"
77. 177
|gene="CES1"
codon_start=1
                                                                                                                                             AB094147.1 GI:30038512
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                            CCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAAAGTACCTGCAG 1650
                                                     bp mRNA linear MAM 09-JUN-2001 for carboxylesterase D1, complete cds.
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QPVAVFLGVPFAKPPLGPLRPAPPQAAEPWNFWTHTSYPPMCSQDAVGGQVLSELFT
NRKDNIPLRFKSEDCLYLNIYTPADLTTXNSRLPVKWHIHGGGLVVGGASTYDGLALSAH
BNVVVYTIQYRLGISPFSTGENGTWGHLDQLAALRWVQENIANFGGNPGSVTIF
GESAGGESVSTUVLSPLAKNLFHRAISESGYALTAALVKKDMKDTAQQLAVFAGCKST
TSAVLYHCLRQKTEDELLEVSLKLKFFTLDLFGDPRESYPFLFTVVDGVLLPKRPQEI
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LIPAASEKYLGGTDDPWKKALLELDMGDVVFGVSVTVARHRDAGAFTYMTBEQYH
PSFSSDMKDQTVVGDPHGDELFSYFGAPFLKGGASEEETRLSKMMKLMANFARSGNPM
GEGLPSWPAYDQKEGYLQ1G1PTQPAQKLKSKEMAFWTELLAKRAAEKLSPTEHVEL
GAGATCAGACTCAGCAAGACGATGATGAAATTTTGGGCCAATTTTGCTCGGAGTGGGAAC 1597
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                                                                                                        1658 ATTGGAGCCACTACTCAGCCGGCCCAGAAGCTGAAAGACAAGGAAGTGGCTTTCTGGA 1715
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (sites)
                                                                                     1651 CTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTGGA 1708
                                                                                                                                                                                                                                                                                                                                                                     dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (11-FEB-1999) Masakiyo Hosokawa, Chiba University, Faculty of Pharmaceutical Sciences; 1-33 Yayoi-cho, Chiba, Chiba 263-8522, Japan (E-mail:masakiyo@p.chiba-u.ac.jp, Tel:81-43-290-2921, Fax:81-43-290-2921)
Location/Qualifiers
1. 1923
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Canis, familiaris
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/note="Dog liver carboxylesterase
/codon_start=1
/product="carboxylesterase D1"
/protein_id="BAB60696.1"
/db_xref="GI:14331125"
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.larity 56.5%; Pred. No. 3.6e-82;
Conservative 0; Mismatches 657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
                                                                                                                                                                                        AB023629 1923
Canis familiaris CESdD1 mRNA
AB023629
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7. .1704
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Direct Submission
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GESAGGGSVS1LLLSPLTKNLFHRAISESGVALLSSLFRKNTKSLAEKIAIEBAGCKTT
TSAVMVHCLROKTEEELMEVTLKMKFMALDLVGDPKENTAFLTTVIDGVLLPKAPABI
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ELTPVATEKYLGGTDDPVKKKDLFLDMLADLLFGVPSVNVARHHRDAGAPTYMYEYRY
RPSPSSDMRPKTVIGDHGDEIFSVLGAPFLKEGATEEEIKLSKNVMKYWANFARNGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                               CCATCCGTGACTGTAGCCCGTCACCACAGAGATGCCGGAGCCCCCACCTACATGTATGAG
                                                                                                                                                                                                                                                                                                                                                                       CCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAAAAGTACCTGCAG
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                                                            TITGAGCACCACGCTCG----TGGAATAATCGTCAAACCCCGCACTGATGGGGCAGACCAT
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Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
1 (bases 1 to 1717)
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Arganism="Oryctolagus on mol type=""RNA"
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Lissue_type="liver"
11. .1708
/EC_number="3.1.1.1"
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Oryctolagus cuniculus
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AF036930
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MEDLINE
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 21 Row: m Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16905523. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTSAVMVHCLROKTEEELLETTLKWKFLSLDLOGDPRESOPLIGTVIOGMLLIKTPEE
LOAERNFHTVPYMVGINKOEFGWLIPWLMSYPLSEGOLDOKTAMSLLMKSYPLVCIAK
ELIPEATEKYLGGTDDTVKKKDLFLDLIADVMFGVPSVIVARNHRDAGAPTYMYEFQY
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NGEGLPHWPEYNQKEGYLQIGANTQAAQKLKDKEVAFWTNLFAKKAVEKPPQTEHIEL
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NKEKBNELKSBDCLYLINIYTPADLTKKNRLPWNVWIHGGGSIMVGAASGTYDGLALAAH
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GESAGGESVYLVLSPPAKNLFHRAISESGYALTSVLKKGDVKPLAEQIAITAGCKT
                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTP/DTP/Gazdar
Tissue Procurement: DCTP/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
Contact: mgGDcm trmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
KOWIS, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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                                                                                                                                                                                                                                                            Direct Submission
Submitted (15-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDMA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/doing="mRNA"
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/note="blide"/forcoor: pCMV-SPORT6"
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/note="COesterase; Region: Carboxylesterase"
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Pred. No. 2.6e-81;
0; Mismatches 632;
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/db_xref="LocusID:1066"
/db_xref="MIM:114835"
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Best Local Similarity 57.1%;
Matches 862; Conservative (
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1 (bases 1 to 1975)

2 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Rlausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,

Biatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Boask, S.A., Mckwan, P.J.,

McKernan, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Wazny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Butfard, G.G., Blakesley, R.W., Towohman, J.W., Genen, E.D.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
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                                                                                             CCACTCTCTGAAGGCAAACTGGACCAGAAGACAGCTACAGAACTCTTGTGGGAAGTCCTAC 1165
                                                                                                                                                                                                                             CCCATTGTCAATGTCTTTAAGGAGCTGACTCCAGTGGCCACTGAGAAGTATTTAGGAGGG 1225
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                                                                                                                                                                                                                                                                                                                                                                                                                       1342 ACTITICGEGRAFIGCCACACTGCACACTGCTCACTACCACCGAGATGCCGGCCTCCCTGTC 1401
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                                  CTAAACCGGCAGGCGA---TGAGAAAGGAAACCATCACTAAGATGCTCTGGAGTACCCGC 1221
                                                                                                                                                              1222 ACCCTGTTGAATATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGAGTACCTGGACAAT 1281
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Homo sapiens carboxylesterase 1 (monocyte/macrophage serine esterase 1), mRNA (cDNA clone MGC:9220 IMAGE:3879691), complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1460 GCCACAGAAGAAGGAGATCAAACTGAGCAAGATGGTGATGAAATACTGGGCCAACTTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCACAGGAAACCCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAAGGATGAA
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